

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 23, 2003, 12:06:52 ; Search time 172.986 Seconds
(without alignments)
3059.318 Million cell updates/sec

Title: US-09-198-779b-1

Perfect score: 235
Sequence: 1 gtttcgcgtcagctcgtcgt.....ctgcgaggtgtgcaagcccc 235

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : N.Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	51.5	2061	21	AAA48574
2	75.6	32.2	1674	21	AAC47744
3	65.8	28.0	1380	20	AAK07185
4	61.6	26.2	1182	19	AAT99143
5	61	26.0	1182	19	AAT99141
6	59.4	25.3	1182	19	AAT99142
7	54.6	23.2	399	20	AAK81128
8	53	22.6	1485	20	AAK07184
9	53	22.6	1518	21	AAA51037

10	51	21.7	1582	20	AAK07183	Corn S-adenosylmet
11	50.4	21.4	635	21	AAC44219	Arabidopsis thalia
12	50.4	21.4	1508	21	AAC33986	Arabidopsis thalia
13	50.4	21.4	1521	21	AAC45478	Arabidopsis thalia
14	50.4	21.4	1529	21	AAC33535	Arabidopsis thalia
15	49.8	21.2	1653	21	AAC45944	Arabidopsis thalia
16	49.8	21.2	1654	21	AAC35348	Arabidopsis thalia
17	46.6	19.8	1636	22	AAD02296	Nicotiana tabacum
18	42.4	18.0	1393	21	AAC46421	Arabidopsis thalia
19	42.4	18.0	1393	21	AAC33674	Arabidopsis thalia
20	40.2	17.1	1208	15	AA064204	snac gene encoding
21	40.2	17.1	5392	15	AA064201	Sequence comprisin
22	40	17.0	4848	24	AAD22684	Streptomyces fridi
23	40	17.0	4848	24	AAD22686	Streptomyces fridi
24	39.4	16.8	1693	21	AAK75637	Nucleotide sequenc
25	39.4	16.8	1693	21	AAZ56005	Contig 004 from co
26	37.4	15.9	297	24	ABL72111	Corn tassell-derive
27	34.6	14.7	56485	21	AAK81476	N. meningitidis pa
28	34.6	14.7	349980	21	AAK21612	N. meningitidis pa
29	34.6	14.7	837096	21	AAA81489	N. meningitidis pa
30	34.4	14.6	4403765	22	AA199683	Mycobacterium tube
31	34.4	14.6	4411529	22	AA199682	Mycobacterium tube
32	33	14.0	17512	23	ABL09034	Drosophila melanog
33	31.2	13.3	1844	22	AAH99804	Human protein enco
34	30.8	13.1	66788	23	AAH59515	Propionibacterium
35	30.6	13.0	606	23	AAH51580	Pseudomonas aerugi
36	30.6	13.0	657	21	AAK12426	Aspergillus oryzae
37	30.6	13.0	2247	23	ABL29661	Drosophila melanog
38	30.2	12.9	566	21	AAK08527	Fusarium venenatum
39	29.8	12.7	1519	20	AAV64373	GABA-gated chlorid
40	29.6	12.6	3550	23	ABL09035	Drosophila melanog
41	29.4	12.5	1683	18	AAT86246	cDNA encoding mugw
42	29.2	12.4	1557	21	AAZ49567	Matz M109 protein
43	29.2	12.4	2604	21	AAA48576	cDNA encoding whea
44	29	12.3	1086	23	ABL04431	Drosophila melanog
45	29	12.3	1221	22	AAH66738	C glutamincum codin
46	29	12.3	1239	16	AAK04566	S-adenosylmethioni
47	29	12.3	1344	22	AAK71873	Corynebacterium gl
48	29	12.3	1344	23	AAK96132	C. glutamincum gene
49	29	12.3	3205	23	ABL04430	Drosophila melanog
50	29	12.3	349980	22	AAH68529	C glutamincum codin

ALIGNMENTS

RESULT 1
ID AAA48574 Standard; cDNA: 2061 BP.

AC AAA48574;
DT 19-SEP-2000 (first entry)

DE cDNA encoding corn protein phosphatase 2A regulatory subunit A.
XX
KW Corn; protein phosphatase 2A; protein phosphorylation modulation;
KW transgenic plant; gene therapy; ss.
XX

OS Zea mays.

FH Key Location/Qualifiers
FT CDS 56..1820
FT /*tag= a
FT /*product= "protein phosphatase 2A regulatory
subunit A"

PN WO200036121-A2.
XX
PD 22-JUN-2000.
XX
PF 15-DEC-1999; 99WO-US29823.
XX

PR	12-OCT-1999;	9905-0158369.
PR	13-OCT-1999;	9905-0159293.
PR	13-OCT-1999;	9905-0159294.
PR	13-OCT-1999;	9905-0159295.
PR	14-OCT-1999;	9905-0159329.
PR	14-OCT-1999;	9905-0159330.
PR	14-OCT-1999;	9905-0159331.
PR	14-OCT-1999;	9905-0159637.
PR	14-OCT-1999;	9905-0159638.
PR	18-OCT-1999;	9905-0159584.
PR	21-OCT-1999;	9905-0160741.
PR	21-OCT-1999;	9905-0160767.
PR	21-OCT-1999;	9905-0160768.
PR	21-OCT-1999;	9905-0160770.
PR	21-OCT-1999;	9905-0160814.
PR	21-OCT-1999;	9905-0160815.
PR	22-OCT-1999;	9905-0160980.
PR	22-OCT-1999;	9905-0160981.
PR	22-OCT-1999;	9905-0160989.
PR	25-OCT-1999;	9905-0161404.
PR	25-OCT-1999;	9905-0161405.
PR	25-OCT-1999;	9905-0161406.
PR	26-OCT-1999;	9905-0161359.
PR	26-OCT-1999;	9905-0161360.
PR	26-OCT-1999;	9905-0161361.
PR	28-OCT-1999;	9905-0161920.
PR	28-OCT-1999;	9905-0161992.
PR	28-OCT-1999;	9905-0161993.
PR	29-OCT-1999;	9905-0162142.

	Query Match	32.2%	Score 75.6;	DB 21;	Length 1674;	
	Best Local Similarity	65.5%;	Pred. No. 1.1e-15;			
	Matches 78; Conservative	0;	Mismatches 41;	Indels	0;	Gaps 0;
OY	117	ACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAGACCGC	176			
		I I				
Dd	1145	AGGATGTGCACCATCACTCGACCTCAAGAAGGGCGGACACAGGTTCATCAGACCGC	1204			
OY	177	CGCATACGCCACTTGGCCCGTGACGACGCCGACTTCACCTCGAGGTTGTAACCCC	235			
Dd	1205	CGCATACGCCACTTGGCCCGTGACGACGCCGACTTCACCTCGAGGTTGTAACCCC	1263			
RESULT 3						
AAx07185						
ID	AAx07185 standard; cDNA; 1380 BP.					
XX						
AC	AAx07185;					
XX						
DT	21-MAY-1999 (first entry)					
XX						
DE	wheat S-adenosylmethionine synthetase cDNA contig.					
XX						
KW	S-adenosylmethionine synthetase; wheat; amino acid; lysine;					
KM	threonine; methionine; cysteine; isoleucine; transgenic plant;					
KW	crop improvement; food; feedstuff; ss.					
XX						
OS	Triticum aestivum.					
XX						
FH	Key	Location/Qualifiers				
FT	CDS	73..1257				
XX		/tag= a				
PN	W09855601-A2.					
XX						
PD	10-DEC-1998.					
XX						
PF	05-JUN-1998;	98WO-US11692.				
XX						
PR	12-JUN-1997;	97US-0048443.				
PA	06-JUN-1997;	97US-0048771.				
(DUPO) DU PONT DE NEMOURS & CO E.I.						

XX Abell LM, Allen SM, Falco SC, Hitz WD, Kinney AJ;
 PI Rafalski JA, Thorpe CJ;
 XX WPI: 1999-070263/06.
 DR P-PSDB: AAM97744.
 XX
 PT New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
 PT encode: dihydropicolinate reductase; diaminopimelate epimerase;
 PT threonine synthase; threonine deaminase; S-adenosylmethionine
 PT synthetase
 XX
 PS Claim 47; Page 69-70; 98pp; English.
 XX
 CC This is the nucleotide sequence of a cDNA contig that codes for
 CC a full-length wheat S-adenosylmethionine synthetase (see AAM97744).
 CC The contig was assembled from clones isolated from wheat kernel.
 CC leaf, seedling and root cDNA libraries and identified by comparison
 CC to public sequence databases using BLAST algorithms. It shows
 CC sequence similarity to the barley enzyme. The invention relates to
 CC new isolated nucleic acid fragments (see AAX07168-85) encoding plant
 CC enzymes (see AAM97727-44) that catalyze steps in the biosynthesis of
 CC lysine, threonine, methionine, cysteine and isoleucine from
 CC aspartate, the enzyme being selected from dihydropicolinate reductase,
 CC diaminopimelate epimerase, threonine synthase, threonine deaminase
 CC or S-adenosylmethionine synthetase. The invention also relates to
 CC the construction of a chimeric gene encoding all or a portion of
 CC the biosynthetic pathway enzyme, in sense or antisense orientation,
 CC where expression of the chimeric gene results in production of
 CC altered levels of the enzyme in a transformed host cell.
 CC Overexpression or reduction of expression of genes encoding the
 CC amino acid biosynthetic pathway enzymes in crop plants such as
 CC corn, soybean and wheat can be used to alter levels of the amino
 CC acids in human food and animal feed. Transformed host cells can
 CC also be used to identify compounds that inhibit one of the enzymes.
 XX
 SO Sequence 1380 BP; 299 A; 430 C; 379 G; 267 T; 5 other;

Query Match 28.0%; Score 65.8; DB 20; Length 1380;
 Best Local Similarity 90.9%; Pred. No. 2.4e-12;
 Matches 70; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 159 CAGGTCATCAAGACCGCCGATAGCGCCTTGCGCGGTAGCGCGGCACTTCACTG 218
 |||||||
 DB 1155 CAGGTCATCAAGACCGCGCTTACGTCCTTGCGCGGTAGCGCGGCACTTCACTG 1214
 |||||||
 OY 219 CGAGGTGCTCAAGCCCC 235
 |||||||
 DB 1215 GGAGGTGCTGAAGCCCC 1231

RESULT 4
 AAT99143
 ID AAT99143 standard; cDNA to mRNA; 1182 BP.
 XX
 AC AAT99143;
 XX
 DT 26-MAR-1998 (first entry)
 XX
 DE S-adenosylmethionine synthase 3 gene.
 XX
 KW S-adenosylmethionine synthase 3 gene; barley; alkali resistant plant;
 KW sam3; ss.
 XX
 OS Hordeum vulgare.
 OS
 PN JP09313186-A.
 XX
 PD 09-DEC-1997.
 XX
 PF 28-MAY-1996; 96JP-0133406.
 XX
 PR 28-MAY-1996; 96JP-0133406.

XX (NIOC) NIPPON OIL CO LTD.
 PA
 XX WPI: 1998-080077/08.
 DR P-PSDB: AAM34542.
 XX
 PT S-adenosyl-methionine synthase gene - useful in producing plants
 PT resistant to alkaline soil
 XX
 PS Claim 6; Page 10-11; 13pp; Japanese.
 XX
 CC This sequence represents the S-adenosylmethionine synthase 3 (sam3)
 CC gene. This DNA sequence may be used in a vector to produce plants which
 CC are resistant to alkaline soil.
 XX
 SO Sequence 1182 BP; 253 A; 368 C; 331 G; 230 T; 0 other;

Query Match 26.2%; Score 61.6; DB 19; Length 1182;
 Best Local Similarity 88.2%; Pred. No. 6.3e-11;
 Matches 67; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 160 AGGTCATCAAGACCGCCGATAGCGCCTTGCGCGGTAGCGCGGCACTTCACTG 219
 |||||||
 DB 1084 AGGTCATCAAGACCGCTGCTTATGTCCTTTGGCGCGGATGCGCACTTCACTG 1143
 |||||||
 OY 220 GAGGTGCTCAAGCCCC 235
 |||||||
 DB 1144 GAGGTGCTGAAGCCCC 1159

RESULT 5
 AAT99141
 ID AAT99141 standard; cDNA to mRNA; 1182 BP.
 XX
 AC AAT99141;
 XX
 DT 26-MAR-1998 (first entry)
 XX
 DE S-adenosylmethionine synthase 1 gene.
 XX
 KW S-adenosylmethionine synthase 1 gene; barley; alkali resistant plant;
 KW sam1; ss.
 XX
 OS Hordeum vulgare.
 OS
 PN JP09313186-A.
 XX
 PD 09-DEC-1997.
 XX
 PF 28-MAY-1996; 96JP-0133406.
 XX
 PR 28-MAY-1996; 96JP-0133406.
 XX
 PA (NIOC) NIPPON OIL CO LTD.
 XX
 DR WPI: 1998-080077/08.
 DR P-PSDB: AAM34540.
 XX
 DE S-adenosyl-methionine synthase gene - useful in producing plants
 PT resistant to alkaline soil
 XX
 PS Claim 4; Page 8-9; 13pp; Japanese.
 XX
 CC This sequence represents the S-adenosylmethionine synthase 1 (sam1)
 CC gene. This DNA sequence may be used in a vector to produce plants which
 CC are resistant to alkaline soil.
 XX
 SO Sequence 1182 BP; 253 A; 372 C; 324 G; 233 T; 0 other;

Query Match 26.0%; Score 61; DB 19; Length 1182;
 Best Local Similarity 87.0%; Pred. No. 1e-10;
 Matches 67; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 159 CAGGTTTCATCAGACCGCCGATACGGCCACTTTGGCCGTGACGAGCCGCACTTCACCTG 218
 |||||||
 DB 1083 CAGGTTTCATCAGACGAGCTGCTTACGGTCACTTTGGCCGCGATGATGCTGACTTCACCTG 1142
 |||||||
 QY 219 CGAGGTGCTCAAGCCCC 235
 |||||||
 DB 1143 GGAGGTGCTGAAGCCCC 1159

RESULT 6
 AAT99142
 ID AAT99142 standard; cDNA to mRNA; 1182 BP.
 XX
 AC AAT99142;
 XX
 DT 26-MAR-1998 (first entry)
 XX
 DE S-adenosylmethionine synthase 2 gene.
 XX
 KW S-adenosylmethionine synthase 2 gene; barley; alkali resistant plant;
 KW sam2; ss.
 XX
 OS Hordeum vulgare.
 XX
 PM JP09313186-A.
 XX
 PD 09-DEC-1997.
 XX
 PF 28-MAY-1996; 96JP-0133406.
 XX
 PR 28-MAY-1996; 96JP-0133406.
 XX
 PA (NIOC) NIPPON OIL CO LTD.
 XX
 DR WPI: 1998-080077/08.
 DR P-PSDB: AAM34541.

PT S-adenosyl-methionine synthase gene - useful in producing plants
 PR resistant to alkaline soil
 XX
 PS Claim 5; Page 9-10; 13pp; Japanese.
 CC This sequence represents the S-adenosylmethionine synthase 2 (sam2)
 CC gene. This DNA sequence may be used in a vector to produce plants which
 CC are resistant to alkaline soil.
 CC
 SQ Sequence 1182 BP; 261 A; 368 C; 324 G; 229 T; 0 other;

Query Match 25.3%; Score 59.4; DB 19; Length 1182;
 Best Local Similarity 85.7%; Pred. No. 3.6e-10;
 Matches 66; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 159 CAGGTTTCATCAGACCGCCGATACGGCCACTTTGGCCGTGACGAGCCGCACTTCACCTG 218
 |||||||
 DB 1083 CAGGTTTCATCAGACGAGCTGCTTACGGTCACTTTGGCCGCGATGATGCTGACTTCACCTG 1142
 |||||||
 QY 219 CGAGGTGCTCAAGCCCC 235
 |||||||
 DB 1143 GGAGGTGCTGAAGCCCC 1159

RESULT 7
 AAX81128
 ID AAX81128 standard; cDNA; 399 BP.
 XX
 AC AAX81128;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE S-adenosyl methionine (SAM) partial cDNA sequence.
 XX
 KW S-adenosylmethionine synthetase; soybean; amino acid; lysine;
 KW senescence-associated receptor-like protein kinase; sark; sam gene; sag;
 KW senescence-associated gene; plant senescence; promoter; pharmaceutical;

KW plant maturation; S-adenosyl methionine; flower; fruit development; ss.
 XX
 OS Phaseolus vulgaris.
 XX
 PN WO9929159-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 08-DEC-1998; 98WO-US25799.
 XX
 PR 08-DEC-1997; 97US-0067898.
 XX
 PA (VITA-) VITALITY BIOTECHNOLOGIES INC.
 XX
 PI Gepstein S, Hajunoje T, Rosner A;
 XX
 DR WPI: 1999-404873/34.
 DR P-PSDB: AAY21978.
 XX
 PT DNA encoding senescence-associated genes for a senescence
 PT receptor-like protein kinase
 XX
 PS Claim 18; Fig 4; 70pp; English.

CC The invention relates to a senescence-associated receptor-like protein
 CC kinase (sark) gene. The sark gene is a senescence-associated gene (sag)
 CC and is expressed early in the plant senescence process. The sark gene
 CC promoter is useful for driving expression of foreign genes having a
 CC desired product, such as a pharmaceutical, during the process of plant
 CC maturation. The sark gene promoter can be used to drive expression of
 CC resistance genes against pathogens or pests during senescence when the
 CC plant is particularly susceptible to infection or infestation. The sark
 CC gene promoter may also be used to drive expression of a gene encoding an
 CC inhibitor of senescence. Plant senescence may be inhibited by use of
 CC antisense sark constructs. Over expression of the sag genes, using the
 CC sark or sam (S-adenosyl methionine) gene promoters is useful for
 CC induction of early senescence. This is useful to obtain flower or fruit
 CC development prior to specific pest onset, prior to undesirable cross-
 CC fertilization from related crops, at a specific time during storage or
 CC retail, or to avoid development of plant structures that are not of
 CC agronomic importance. The present sequence represents a partial cDNA
 CC clone of S-adenosyl methionine (SAM).

SQ Sequence 399 BP; 108 A; 80 C; 82 G; 129 T; 0 other;
 Query Match 23.2%; Score 54.6; DB 20; Length 399;
 Best Local Similarity 81.8%; Pred. No. 1e-08;
 Matches 63; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 159 CAGGTTTCATCAGACCGCCGATACGGCCACTTTGGCCGTGACGAGCCGCACTTCACCTG 218
 |||||||
 DB 101 CAGGTTCTGTAAGACGCTGCACTATGACACTTCGGCAAGAGAGCGCTGACTTCACATG 160
 |||||||
 QY 219 CGAGGTGCTCAAGCCCC 235
 |||||||
 DB 161 GGAAGGTGCTCAAGCCCC 177

RESULT 8
 AAX07184
 ID AAX07184 standard; cDNA; 1485 BP.
 XX
 AC AAX07184;
 XX
 DT 21-MAY-1999 (first entry)
 XX
 DE Soybean S-adenosylmethionine synthetase cDNA clone s2.12006.
 XX
 KW S-adenosylmethionine synthetase; soybean; amino acid; lysine;
 KW threonine; methionine; cysteine; isoleucine; transgenic plant;
 KW crop improvement; food; feedstuff; ss.
 XX
 OS Glycine max.

XX	Key	Location/Qualifiers
FH	CDS	74..1252
FT		/tag= a
XX		
XX	W09855601-A2.	
PN		
XX	10-DEC-1998.	
PD		
XX		
XX	05-JUN-1998;	98WO-US11692.
PF		
XX	12-JUN-1997;	97US-0049443.
PR	06-JUN-1997;	97US-0048771.
XX		
PA	(DUPO) DU PONT DE NEMOURS & CO E I.	
PB		
PI	Abeil LM, Allen SM, Falco SC, Hitz WD, Kinney AJ;	
PI	Rafalski JA, Thorpe CJ;	
XX		
DR	WPI: 1999-070263/06.	
DR	P-PSDB: AAM97743.	
XX		
PT	New plant amino acid biosynthetic enzymes, DNA and chimeric genes -	
PT	encode: dihydriopicolinate reductase; diamino pimelate epimerase;	
PT	threonine synthase; threonine deaminase; S-adenosylmethionine	
PT	synthetase	
XX		
PS	Claim 44; Page 66-67; 98pp; English.	
XX		
.CC	This is the nucleotide sequence of cDNA clone sz.12b06, which	
.CC	codes for a full-length soybean S-adenosylmethionine synthetase	
.CC	(see AAM97743). The clone was isolated from a soybean seed cDNA	
.CC	library and identified by comparison to public sequence databases	
.CC	using BLAST algorithms. It shows sequence similarity to the	
.CC	tomato enzyme. The invention relates to new isolated nucleic	
.CC	acid fragments (see AAX07168-85) encoding plant enzymes (see	
.CC	AAM97727-44) that catalyze steps in the biosynthesis of lysine,	
.CC	threonine, methionine, cysteine and isoleucine from aspartate, the	
.CC	enzyme being selected from dihydriopicolinate reductase,	
.CC	diaminopimelate epimerase, threonine synthase, threonine deaminase	
.CC	or S-adenosylmethionine synthetase. The invention also relates to	
.CC	the construction of a chimeric gene encoding all or a portion of	
.CC	the biosynthetic pathway enzyme, in sense or antisense orientation,	
.CC	where expression of the chimeric gene results in production of	
.CC	altered levels of the enzyme in a transformed host cell.	
.CC	Overexpression or reduction of expression of genes encoding the	
.CC	amino acid biosynthetic pathway enzymes in crop plants such as	
.CC	corn, soybean and wheat can be used to alter levels of the amino	
.CC	acids in human food and animal feed. Transformed host cells can	
.CC	also be used to identify compounds that inhibit one of the enzymes.	
XX		
SQ	Sequence 1485 BP; 366 A; 373 C; 357 G; 389 T; 0 other;	
Query Match	22.6%;	Score 53; DB 20; Length 1485;
Best Local Similarity	80.5%;	Pred. No. 6, 4e-08;
Matches 62:	Conservative 0;	Mismatches 15; Indels 0; Gaps 0;
OY	159 CAGGTTTCATCAAGACCGCGCATACGGCATTGGCCCTGCAGACGCCACTTCACTTG 218	
Dd		
	1156 CAGGTTCTTGAAGATCGTGCATATGAGACACTTCGGCAGAAGAGACCCTGACTTCATG 1215	
OY	219 CGAGGTGGTCAAGCCCC 235	
Dd	1216 GGAACTGGTCAAGCCCC 1232	
RESULT 9		
ID	AAA51037 standard; cDNA; 1518 BP.	
AAAS1037		
AC	AAA51037;	
DT	09-OCT-2000 (first entry)	

```

XX soybean S-adenosyl-L-methionine synthetase cDNA.
XX
XX S-adenosyl-L-methionine synthetase; SAMS; probe: promoter; embryo;
XX constitutive; tissue-specific; development-specific;
XX herbicide resistance; pathogen resistance; ss.
XX
XX Glycine max.
XX
XX Key Location/Qualifiers
XX 5'UTR 1..73
XX FT /*tag= a
XX FT 74..1252
XX CDS /*tag= b
XX /product= S-adenosyl-L-methionine_Synthetase
XX
XX WO200037662-A2.
XX
XX 29-JUN-2000.
XX
XX 17-DEC-1999; 99WO-US30180.
XX
XX 21-DEC-1998; 98US-0113045.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Falco SC, Ll Z;
XX
XX WPI; 2000-442682/38.
XX
XX S-adenosyl-L-methionine synthetase promoter for expressing target
XX heterologous herbicide-resistance or pathogen-resistance nucleic acid
XX fragments in plants, especially soybean
XX
XX Example 2; Page 39; 50pp; English.
XX
XX This is the soybean full-length S-adenosyl-L-methionine synthetase (SAMS)
XX cDNA, which was used to generate a probe to isolate a SAMS promoter. The
XX SAMS promoter is active in seedlings and callus and over-expression of a
XX gene in embryo stage can be achieved at an early developing stage using
XX the SAMS promoter. The SAMS promoter may be used as an alternative to
XX cauliflower mosaic virus 35S promoter to drive expression of selectable
XX marker genes. Plant cells transformed with the SAMS constitutive promoter
XX are useful for increasing or decreasing the expression of heterologous
XX nucleic acid fragments in a plant, preferably corn, rice, wheat, barley,
XX palm, Arabidopsis, soybean, oil seed Brassica, peanut, sunflower,
XX safflower, cotton, tobacco, tomato, potato or cocoa. Target heterologous
XX nucleic acid fragments include herbicide or pathogen resistance
XX
XX Sequence 1518 BP; 399 A; 373 C; 357 G; 389 T; 0 other:
XX
XX Query Match 22.6%; Score 53; DB 21; Length 1518;
XX Best Local Similarity 80.5%; Pred. No. 6.5e-08;
XX Matches 62; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
XX
XX 159 CAGGTTTCATCAAGACCGCGCATACGGCCATTGGCCGTCGACGACCGCATTTACCTG 218
XX ||||||| 11111 11 11111 11 1111 11 11 111 11111111 11
XX Db 1156 CAGGTTCTTGAAGACTGCTGCATATGACACTCGCAGAGAGACCCGACTTCACATG 1215
XX
XX 219 CGAGTGGTCMAAGCCCC 235
XX || |||||
XX Db 1216 GGAAGTGGTCAGAGCCCC 1232
XX
XX RESULT 10
XX AAX07183
XX ID AAX07183 standard; cDNA: 1582 BP.
XX
XX AC AAX07183;
XX
XX 21-MAY-1999 (first entry)
XX

```

DE Corn S-adenosylmethionine synthetase cDNA clone cc3.mn0002.d2.
 XX
 KW S-adenosylmethionine synthetase; corn; maize; amino acid; lysine;
 KW threonine; methionine; cysteine; isoleucine; transgenic plant;
 KW crop improvement; food; feedstuff; ss.
 XX
 OS Zea mays.
 XX
 FH Key Location/Qualifiers
 FT CDS 140..1330
 FT /*tag= a
 XX
 PN MO9855601-A2.
 XX
 PD 10-DEC-1998.
 XX
 PE 05-JUN-1998; 98WO-US11692.
 XX
 PR 12-JUN-1997; 97US-0049443.
 PR 06-JUN-1997; 97US-0048771.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX
 PI Abell LM, Allen SM, Falco SC, Hitz WD, Kinney AJ;
 PI Rafalski JA, Thorpe CJ;
 XX
 DR WPI: 1999-070263/06.
 DR P-PSDB; AAW97742.
 XX
 PT New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
 PT encode: dihydropicolinate reductase; diaminopimelate epimerase;
 PT threonine synthase; threonine deaminase; S-adenosylmethionine
 PT synthetase
 XX
 PS Claim 41; Page 62-63; 98pp; English.
 XX
 CC This is the nucleotide sequence of cDNA clone cc3.mn0002.d2, which
 CC codes for a full-length corn S-adenosylmethionine synthetase
 CC (see AAW97742). The clone was isolated from a corn callus cDNA
 CC library and identified by comparison to public sequence databases
 CC using BLAST algorithms. It shows sequence similarity to the
 CC Oryza sativa enzyme. The invention relates to new isolated
 CC nucleic acid fragments (see AAX07168-85) encoding plant enzymes (see
 CC AAW97727-44) that catalyze steps in the biosynthesis of lysine,
 CC threonine, methionine, cysteine and isoleucine from aspartate, the
 CC enzyme being selected from dihydropicolinate reductase,
 CC diaminopimelate epimerase, threonine synthase, threonine deaminase
 CC or S-adenosylmethionine synthetase. The invention also relates to
 CC the construction of a chimeric gene encoding all or a portion of
 CC the biosynthetic pathway enzyme, in sense or antisense orientation,
 CC where expression of the chimeric gene results in production of
 CC altered levels of the enzyme in a transformed host cell.
 CC Overexpression or reduction of expression of genes encoding the
 CC amino acid biosynthetic pathway enzymes in crop plants such as
 CC corn, soybean and wheat can be used to alter levels of the amino
 CC acids in human food and animal feed. Transformed host cells can
 CC also be used to identify compounds that inhibit one of the enzymes.
 CC
 XX
 S0 Sequence 1582 BP; 340 A; 474 C; 417 G; 351 T; 0 other:
 Query Match 21.7%; Score 51; DB 20; Length 1582;
 Best Local Similarity 80.0%; Pred. No. 3.2e-07;
 Matches 60; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 Oy 161 GGTTCATCAAGACCGCCGATACGGCCACTTGGCCGTCAGACGCCCACTTCACCTCG 220
 Db 1230 GCTTACTCTAAGACGGCAGCCTTACGCGCACTTCGGAAGGAGACGCCCTACTTCACCTCG 1289
 Oy 221 AGGTGTCAGCCCC 235
 Db 1290 AGGTGTCAGCCAC 1304

RESULT 11
 AAC44219
 ID AAC44219 standard; DNA; 635 BP.
 XX
 AC AAC44219;
 XX
 DT 18-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 42062.
 XX
 KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PE 25-FEB-2000; 2000EP-0301439.
 XX
 PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130444.
 PR 23-APR-1999; 99US-0130510.
 PR 28-APR-1999; 99US-0130891.
 PR 30-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 04-MAY-1999; 99US-0132407.
 PR 05-MAY-1999; 99US-0132484.
 PR 06-MAY-1999; 99US-0132485.
 PR 06-MAY-1999; 99US-0132486.
 PR 06-MAY-1999; 99US-0132487.
 PR 07-MAY-1999; 99US-0132863.
 PR 11-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134218.
 PR 14-MAY-1999; 99US-0134219.
 PR 14-MAY-1999; 99US-0134221.
 PR 14-MAY-1999; 99US-0134370.
 PR 18-MAY-1999; 99US-0134766.
 PR 19-MAY-1999; 99US-0134941.
 PR 20-MAY-1999; 99US-0135124.
 PR 21-MAY-1999; 99US-0135353.
 PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139492.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.

PR	18-JUN-1999;	99US-0139459;	PR	20-AUG-1999;	99US-0149929;
PR	18-JUN-1999;	99US-0139460;	PR	23-AUG-1999;	99US-0149902;
PR	18-JUN-1999;	99US-0139461;	PR	23-AUG-1999;	99US-0149930;
PR	18-JUN-1999;	99US-0139462;	PR	25-AUG-1999;	99US-0150566;
PR	18-JUN-1999;	99US-0139463;	PR	26-AUG-1999;	99US-0150884;
PR	18-JUN-1999;	99US-0139750;	PR	27-AUG-1999;	99US-0151065;
PR	18-JUN-1999;	99US-0139763;	PR	27-AUG-1999;	99US-0151066;
PR	21-JUN-1999;	99US-0139817;	PR	27-AUG-1999;	99US-0151080;
PR	22-JUN-1999;	99US-0139899;	PR	30-AUG-1999;	99US-0151303;
PR	23-JUN-1999;	99US-0140353;	PR	31-AUG-1999;	99US-0151308;
PR	23-JUN-1999;	99US-0140354;	PR	01-SEP-1999;	99US-0151930;
PR	24-JUN-1999;	99US-0140695;	PR	07-SEP-1999;	99US-0152363;
PR	28-JUN-1999;	99US-0140823;	PR	10-SEP-1999;	99US-0153070;
PR	29-JUN-1999;	99US-0140991;	PR	13-SEP-1999;	99US-0153758;
PR	30-JUN-1999;	99US-0141287;	PR	15-SEP-1999;	99US-0154018;
PR	01-JUL-1999;	99US-0141842;	PR	16-SEP-1999;	99US-0154039;
PR	01-JUL-1999;	99US-0142154;	PR	20-SEP-1999;	99US-0154779;
PR	02-JUL-1999;	99US-0142055;	PR	22-SEP-1999;	99US-0155139;
PR	06-JUL-1999;	99US-0142390;	PR	23-SEP-1999;	99US-0155486;
PR	08-JUL-1999;	99US-0142803;	PR	24-SEP-1999;	99US-0155659;
PR	09-JUL-1999;	99US-0142920;	PR	28-SEP-1999;	99US-0156458;
PR	12-JUL-1999;	99US-0142977;	PR	29-SEP-1999;	99US-0156596;
PR	13-JUL-1999;	99US-0143542;	PR	04-OCT-1999;	99US-0157117;
PR	14-JUL-1999;	99US-0143624;	PR	05-OCT-1999;	99US-0157753;
PR	15-JUL-1999;	99US-0144005;	PR	06-OCT-1999;	99US-0157865;
PR	16-JUL-1999;	99US-0144085;	PR	07-OCT-1999;	99US-0158029;
PR	16-JUL-1999;	99US-0144086;	PR	08-OCT-1999;	99US-0158232;
PR	19-JUL-1999;	99US-0144325;	PR	12-OCT-1999;	99US-0158369;
PR	19-JUL-1999;	99US-0144331;	PR	13-OCT-1999;	99US-0159293;
PR	19-JUL-1999;	99US-0144332;	PR	13-OCT-1999;	99US-0159284;
PR	19-JUL-1999;	99US-0144333;	PR	13-OCT-1999;	99US-0159295;
PR	19-JUL-1999;	99US-0144334;	PR	14-OCT-1999;	99US-0159329;
PR	20-JUL-1999;	99US-0144352;	PR	14-OCT-1999;	99US-0159330;
PR	20-JUL-1999;	99US-0144632;	PR	14-OCT-1999;	99US-0159331;
PR	20-JUL-1999;	99US-0144684;	PR	14-OCT-1999;	99US-0159637;
PR	21-JUL-1999;	99US-0144814;	PR	18-OCT-1999;	99US-0159638;
PR	21-JUL-1999;	99US-0145086;	PR	18-OCT-1999;	99US-0159584;
PR	21-JUL-1999;	99US-0145088;	PR	21-OCT-1999;	99US-0160741;
PR	22-JUL-1999;	99US-0145085;	PR	21-OCT-1999;	99US-0160767;
PR	22-JUL-1999;	99US-0145087;	PR	21-OCT-1999;	99US-0160768;
PR	22-JUL-1999;	99US-0145089;	PR	21-OCT-1999;	99US-0160770;
PR	22-JUL-1999;	99US-0145192;	PR	21-OCT-1999;	99US-0160814;
PR	23-JUL-1999;	99US-0145145;	PR	21-OCT-1999;	99US-0160815;
PR	23-JUL-1999;	99US-0145218;	PR	22-OCT-1999;	99US-0160980;
PR	23-JUL-1999;	99US-0145224;	PR	22-OCT-1999;	99US-0160981;
PR	26-JUL-1999;	99US-0145276;	PR	22-OCT-1999;	99US-0160989;
PR	27-JUL-1999;	99US-0145913;	PR	25-OCT-1999;	99US-0161404;
PR	27-JUL-1999;	99US-0145918;	PR	25-OCT-1999;	99US-0161405;
PR	27-JUL-1999;	99US-0145919;	PR	25-OCT-1999;	99US-0161406;
PR	28-JUL-1999;	99US-0145951;	PR	26-OCT-1999;	99US-0161359;
PR	02-AUG-1999;	99US-0146386;	PR	26-OCT-1999;	99US-0161360;
PR	02-AUG-1999;	99US-0146388;	PR	28-OCT-1999;	99US-0161361;
PR	03-AUG-1999;	99US-0146389;	PR	28-OCT-1999;	99US-0161920;
PR	03-AUG-1999;	99US-0147038;	PR	28-OCT-1999;	99US-01

XX AAC33986;
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 5035.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 23-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 23-APR-1999; 99US-0130891.
XX 28-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 30-APR-1999; 99US-0132407.
XX 04-MAY-1999; 99US-0132484.
XX 05-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 07-MAY-1999; 99US-0132487.
XX 11-MAY-1999; 99US-0134256.
XX 14-MAY-1999; 99US-0134218.
XX 14-MAY-1999; 99US-0134219.
XX 14-MAY-1999; 99US-0134221.
XX 18-MAY-1999; 99US-0134370.
XX 19-MAY-1999; 99US-0134768.
XX 20-MAY-1999; 99US-0134941.
XX 21-MAY-1999; 99US-0135124.
XX 21-MAY-1999; 99US-0135353.
XX 24-MAY-1999; 99US-0135629.
XX 25-MAY-1999; 99US-0136021.
XX 27-MAY-1999; 99US-0136392.
XX 28-MAY-1999; 99US-0136782.
XX 01-JUN-1999; 99US-0137222.
XX 03-JUN-1999; 99US-0137328.
XX 04-JUN-1999; 99US-0137502.
XX 07-JUN-1999; 99US-0137724.
XX 08-JUN-1999; 99US-0138094.
XX 10-JUN-1999; 99US-0138540.
XX 10-JUN-1999; 99US-0138847.
XX 14-JUN-1999; 99US-0139119.
XX 16-JUN-1999; 99US-0139452.
XX 17-JUN-1999; 99US-0139453.
XX 17-JUN-1999; 99US-0139492.
XX 18-JUN-1999; 99US-0139454.
XX 18-JUN-1999; 99US-0139455.
XX 18-JUN-1999; 99US-0139456.
XX 18-JUN-1999; 99US-0139457.
XX 18-JUN-1999; 99US-0139458.
XX 18-JUN-1999; 99US-0139459.
XX 18-JUN-1999; 99US-0139460.
XX 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142380.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144088.
PR 16-JUL-1999; 99US-0144088.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147316.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148177.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.


```
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149375.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.

PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 21.4%; Score 50.4; DB 21; Length 1521;
Best Local Similarity 78.9%; Pred. No. 5.1e-07;
Matches 60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 160 AGGTCATCAAGACCCGCAATACGCGCATTTGGCCGTGACGACCGCACTTCACTTGC 219
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1168 AGGTCCTTGAGACAGCTGCGCCATGCTATGTGCTACTTTGGAAGGACGATGCTGATTTCACTTGG 1227
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 220 GAGGTGTCAGACCCC 235
      ||||| ||||| ||||| |||||
DB 1228 GAGGTAGTCAGACCCAC 1243

RESULT 14
AAC33535
ID AAC33535 standard; DNA; 1529 BP.
XX
AC AAC33535;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 3408.
```

XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
OS *Arabidopsis thaliana*.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 990S-0121925.
PR 05-MAR-1999; 990S-0123180.
PR 09-MAR-1999; 990S-0123548.
PR 23-MAR-1999; 990S-0125788.
PR 25-MAR-1999; 990S-0126264.
PR 29-MAR-1999; 990S-0126785.
PR 01-APR-1999; 990S-0127462.
PR 06-APR-1999; 990S-0128234.
PR 08-APR-1999; 990S-0128714.
PR 16-APR-1999; 990S-0129845.
PR 19-APR-1999; 990S-0130077.
PR 21-APR-1999; 990S-0130449.
PR 23-APR-1999; 990S-0130510.
PR 28-APR-1999; 990S-0130891.
PR 30-APR-1999; 990S-0131449.
PR 30-APR-1999; 990S-0132048.
PR 04-MAY-1999; 990S-0132407.
PR 05-MAY-1999; 990S-0132484.
PR 06-MAY-1999; 990S-0132485.
PR 06-MAY-1999; 990S-0132486.
PR 07-MAY-1999; 990S-0132487.
PR 11-MAY-1999; 990S-0132863.
PR 14-MAY-1999; 990S-0134218.
PR 14-MAY-1999; 990S-0134219.
PR 14-MAY-1999; 990S-0134221.
PR 14-MAY-1999; 990S-0134370.
PR 18-MAY-1999; 990S-0134768.
PR 19-MAY-1999; 990S-0134941.
PR 20-MAY-1999; 990S-0135124.
PR 21-MAY-1999; 990S-0135353.
PR 24-MAY-1999; 990S-0135629.
PR 25-MAY-1999; 990S-0136021.
PR 27-MAY-1999; 990S-0136392.
PR 28-MAY-1999; 990S-0136782.
PR 01-JUN-1999; 990S-0137222.
PR 03-JUN-1999; 990S-0137528.
PR 04-JUN-1999; 990S-0137502.
PR 07-JUN-1999; 990S-0137724.
PR 08-JUN-1999; 990S-0138094.
PR 10-JUN-1999; 990S-0138540.
PR 10-JUN-1999; 990S-0138847.
PR 14-JUN-1999; 990S-0139119.
PR 16-JUN-1999; 990S-0139423.
PR 16-JUN-1999; 990S-0139432.
PR 17-JUN-1999; 990S-0139452.
PR 18-JUN-1999; 990S-0139454.
PR 18-JUN-1999; 990S-0139455.
PR 18-JUN-1999; 990S-0139456.
PR 18-JUN-1999; 990S-0139457.
PR 18-JUN-1999; 990S-0139458.
PR 18-JUN-1999; 990S-0139459.
PR 18-JUN-1999; 990S-0139460.
PR 18-JUN-1999; 990S-0139461.
PR 18-JUN-1999; 990S-0139462.
PR 18-JUN-1999; 990S-0139463.
PR 18-JUN-1999; 990S-0139750.
PR 18-JUN-1999; 990S-0139763.
PR 21-JUN-1999; 990S-0139817.
PR 22-JUN-1999; 990S-0139899.
PR 23-JUN-1999; 990S-0140353.
PR 23-JUN-1999; 990S-0140354.
PR 24-JUN-1999; 990S-0140695.
PR 28-JUN-1999; 990S-0140823.
PR 29-JUN-1999; 990S-0140991.
PR 30-JUN-1999; 990S-0141287.
PR 01-JUL-1999; 990S-0141842.
PR 01-JUL-1999; 990S-0142154.
PR 02-JUL-1999; 990S-0142055.
PR 06-JUL-1999; 990S-0142390.
PR 08-JUL-1999; 990S-0142803.
PR 09-JUL-1999; 990S-0142920.
PR 12-JUL-1999; 990S-0142977.
PR 13-JUL-1999; 990S-0143542.
PR 14-JUL-1999; 990S-0143624.
PR 15-JUL-1999; 990S-0144005.
PR 16-JUL-1999; 990S-0144085.
PR 16-JUL-1999; 990S-0144086.
PR 19-JUL-1999; 990S-0144325.
PR 19-JUL-1999; 990S-0144331.
PR 19-JUL-1999; 990S-0144332.
PR 19-JUL-1999; 990S-0144333.
PR 19-JUL-1999; 990S-0144334.
PR 19-JUL-1999; 990S-0144335.
PR 20-JUL-1999; 990S-0144632.
PR 20-JUL-1999; 990S-0144884.
PR 21-JUL-1999; 990S-0144814.
PR 21-JUL-1999; 990S-0145086.
PR 21-JUL-1999; 990S-0145088.
PR 22-JUL-1999; 990S-0145085.
PR 22-JUL-1999; 990S-0145087.
PR 22-JUL-1999; 990S-0145089.
PR 22-JUL-1999; 990S-0145192.
PR 23-JUL-1999; 990S-0145145.
PR 23-JUL-1999; 990S-0145218.
PR 23-JUL-1999; 990S-0145224.
PR 26-JUL-1999; 990S-0145276.
PR 27-JUL-1999; 990S-0145593.
PR 27-JUL-1999; 990S-0145598.
PR 27-JUL-1999; 990S-0145599.
PR 28-JUL-1999; 990S-0145951.
PR 02-AUG-1999; 990S-0146386.
PR 02-AUG-1999; 990S-0146388.
PR 02-AUG-1999; 990S-0146389.
PR 03-AUG-1999; 990S-0147038.
PR 04-AUG-1999; 990S-0147204.
PR 04-AUG-1999; 990S-0147302.
PR 05-AUG-1999; 990S-0147182.
PR 05-AUG-1999; 990S-0147260.
PR 06-AUG-1999; 990S-0147303.
PR 06-AUG-1999; 990S-0147416.
PR 09-AUG-1999; 990S-0147493.
PR 09-AUG-1999; 990S-0147935.
PR 10-AUG-1999; 990S-0148171.
PR 11-AUG-1999; 990S-0148319.
PR 12-AUG-1999; 990S-0148341.
PR 13-AUG-1999; 990S-0148565.
PR 13-AUG-1999; 990S-0148684.
PR 16-AUG-1999; 990S-0149368.
PR 17-AUG-1999; 990S-0149175.
PR 18-AUG-1999; 990S-0149426.
PR 20-AUG-1999; 990S-0149722.
PR 20-AUG-1999; 990S-0149723.
PR 20-AUG-1999; 990S-0149929.
PR 23-AUG-1999; 990S-0149902.
PR 23-AUG-1999; 990S-0149930.
PR 23-AUG-1999; 990S-0150366.
PR 26-AUG-1999; 990S-0150884.
PR 27-AUG-1999; 990S-0151065.
PR 27-AUG-1999; 990S-0151066.
PR 27-AUG-1999; 990S-0151080.
PR 30-AUG-1999; 990S-0151303.


```
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156556.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
```

Query Match 21.4%; Score 50.4; DB 21; Length 1529;

Best Local Similarity 78.9%; Pred. No. 5.1e-07; Mismatches 16; Indels 0; Gaps 0;

Matches 60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 160 AGGTTTCATCAGACCGCGCATTCAGGCGCCTTGCGCCGTGACGACGCGGCACTTCACTTCG 219

Db 1210 AGGTTTCGTAAGACGCGCGCTTACGACGACCTTGGAAGACGACCGCGGCACTTCACTTCG 1269

QY 220 GAGGTGTCAGCCCC 235

Db 1270 GAGTGTCAAGCCAC 1285

RESULT 15

AAC45944

ID AAC45944 standard; DNA; 1653 BP.

AC AAC45944;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment seq ID NO: 48340.

DE Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

```
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS EPI033405-A2.
XX 06-SEP-2000.
PD 25-FEB-2000; 2000EP-0301439.
PF 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123160.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
```


XX EP1033405-A2.
XX
XX 06-SEP-2000.
PD
XX 25-FEB-2000; 2000EP-0301439.
PF
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0128845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131448.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145981.
PR 02-AUG-1999; 99US-0145386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148311.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 30-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.

```

PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158368.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162142.

```

```

Query Match 21.2%; Score 49.8; DB 21; Length 1654;
Best Local Similarity 77.9%; Pred. No. 8.5e-07;
Matches 60; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 159 CAGGTTTCATCAAGACCGCGCATACGCCACTTGGCCGTGACAGCGCCGACTTCACCTG 218
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1228 CAGGTTCCAGAAACCGCTGCGTATGCGCATTTCCGCGCTATGACCTGACTTCACCTG 1287
QY 219 CGAGGTGTCAGACCCG 235
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1288 GGAGGTGTCTCAAGCCG 1304

```

```

RESULT 17
AAD02296
ID AAD02296 standard; DNA; 1636 BP.
XX
AC AAD02296;
XX
DT 28-MAR-2001 (first entry)
XX
DE Nicotiana tabacum S-adenosylmethionine synthetase (SAMS) DNA.
XX
KM Tobacco: alkaloid; nicotine; transgenic plant; pharmaceutical protein;
KW herbicide resistance; S-adenosylmethionine synthetase; SAMS; ds.
XX
OS Nicotiana tabacum.
XX
key Location/Qualifiers
FH 96..1268
FT CDS
FT /**tag- a

```

```

FT /product= "Nicotiana tabacum S-adenosylmethionine
FT synthetase (SAMS) protein"
XX
XX WO200067558-A1.
XX
XX 16-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US12450.
XX
XX 06-MAY-1999; 99US-0132919.
XX
XX (TIMK/) TIMKO M.
XX
XX Timko M;
XX
XX WPI: 2001-007279/01.
XX
XX P-PSDB: AAV72078.
XX
XX New nucleic acid encoding alkaloid-synthesis enzymes in tobacco, useful
XX e.g. for producing transgenic plants with altered nicotine content
XX
XX Claim 1; Page 78-79; 103pp; English.
XX
XX The invention relates to enzymes involved in alkaloid, specifically
XX nicotine, synthesis in tobacco and nucleic acids encoding them. The
XX nucleic acid of the invention can be used, in sense or antisense
XX orientation, to produce transgenic tobacco plants with altered
XX alkaloid content, and also for expression of exogenous proteins,
XX e.g. pharmaceutical proteins or proteins implicated in resistance
XX to herbicides. The protein of the invention can be used to
XX identify modulators of enzymatic activity in plants.
XX The present sequence is Nicotiana tabacum S-adenosylmethionine
XX synthetase (SAMS) DNA. This enzyme is involved in the nicotine
XX biosynthetic pathway.
XX
XX Sequence 1636 BP; 444 A; 365 C; 373 G; 454 T; 0 other;

```

```

Query Match 19.8%; Score 46.6; DB 22; Length 1636;
Best Local Similarity 75.3%; Pred. No. 1.1e-05;
Matches 58; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 159 CAGGTTTCATCAAGACCGCGCATACGCCACTTGGCCGTGACAGCGCCGACTTCACCTG 218
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1175 CAGGTACCAAGAGACTGAGCTTATGTCACCTTGGCCGTGATGACCCGACTTCATG 1234
QY 219 CGAGGTGTCAGACCCG 235
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1235 GGAGACTGTCAAGCTC 1251

```

```

RESULT 18
AAC46421
ID AAC46421 standard; DNA; 1393 BP.
XX
AC AAC46421;
XX
XX 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 50076.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.

```

PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132488.
PR 05-MAY-1999; 99US-0132488.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148173.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0153263.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.

PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144332.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145224.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149928.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154038.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.

PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 18.0%; Score 42.4; DB 21; Length 1395;
Best Local Similarity 72.4%; Pred. No. 0.00028;
Matches 55; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 160 AGCTTCATCAGACCGCGCATTCGCGCCGTGACGACGCGCATTCACCTGC 219
Db 1175 AGCTTCAGAAAACGCGACGTGACATTCGAGAGACGACCGCTGACTTCACCTGC 1234
OY 220 GAGGTGTCAGGCC 235
Db 1235 GAGGTGTCAGGCCAC 1250

RESULT 20
AA064204
ID AA064204 standard; CDNA; 1208 BP.

XX AC AA064204;

XX DT 18-NOV-1994 (first entry)

XX DE snac gene encoding enzyme in streptogramin biosynthetic pathway.

XX KW Antibiotic; streptogramin; snac; snab; snac; biosynthesis; enzyme;

XX KM biosynthetic pathway; Streptomyces pristinaespiralis; ds.

XX OS Streptomyces pristinaespiralis.

XX FH Key Location/Qualifiers

FT CDS 1..1209

FT FT /*tag= a

XX PN FR2696189-A.

PD 01-APR-1994.

PF 25-SEP-1992; 92FR-0011441.

XX 25-SEP-1992; 92FR-0011441.

XX (RHON) RHONE POULENC RORER SA.

XX XX

PI Blanc V., Blanche F., Crouzet J., Jacques N., Lacroix P;
PI Thibaut D., Zagorec M;
xx
DR WPI: 1994-128286/16.
P-PSDB; AAR54204.
xx
DNA involved in streptogramin antibiotic biosynthesis - for
PT prodn. or bio-conversion of streptogramin(s) or prodn. of
PT streptogramin intermediates, derivs. or hybrid antibiotics
xx
PS Claim 2; Page 54-55; 83pp; French.

CC The snac gene product is involved in the biosynthesis of
CC streptogramins, antibiotics active against Gram-positive bacteria.
CC The identification of the sequences encoding the enzymes involved
CC in the biosynthetic pathway means that they can be isolated and
CC manipulated. Mutant microorganisms in which a step in the
CC streptogramin biosynthetic pathway is blocked can be cultured to
CC produce streptogramin intermediates, which may later be converted
CC to streptogramin derivatives. Recombinant cells may also be used
CC for the bioconversion of streptogramins from one form to another or
CC for the production of hybrid antibiotics.
xx

SQ Sequence 1208 BP; 190 A; 500 C; 360 G; 158 T; 0 other;

Query Match 17.1%; Score 40.2; DB 15; Length 1208;
Best Local Similarity 46.7%; Pred. No. 0.0015;
Matches 57; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

OY 113 ACGTCAGCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAAGTTCATCACA 172
||| ||
Db 1055 ACCTCGGCCGCGGCATCATCCGGACCTTGACCCTGCTGGGCCCATCTACGGCGCA 1114
||||| ||||||| ||||| || ||||||| ||||| ||| |

OY 173 CCGCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTCGAGTGTCAC 232
||||| ||||||| ||||| || ||||||| ||||| ||| |

Db 1115 CGCGCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTCGAGTGTCAC 1174
||| ||| 233 CC 234
|
Db 1175 GC 1176

RESULT 21
AAO64201
ID AAO64201 standard; cDNA: 5392 BP.

XX AAO64201;
AC XX
CC XX
DT DT 18-NOV-1994 (first entry)
XX XX
DE Sequence comprising the snac, snab and snac gene cluster.
XX XX
KW Antibiotic; streptogramin; snac; snab; snac; biosynthesis; enzyme;
KM biosynthetic pathway; Streptomyces pristinaespiralis; ds.
OS Streptomyces pristinaespiralis.
XX XX
PN FR2696189-A.
XX XX
PD 01-APR-1994.
XX XX
PF 25-SEP-1992; 92FR-0011441.
XX XX
PR 25-SEP-1992; 92FR-0011441.
XX XX
PA (RHON) RHONE POULENC RORER SA.
XX XX
PI Blanc V., Blanche F., Crouzet J., Jacques N., Lacroix P;
PI Thibaut D., Zagorec M;
xx
DR WPI: 1994-128286/16.
xx
TF DNA involved in streptogramin antibiotic biosynthesis - for

[illegible]

[illegible]

PS	Claim 19; Column 31-36; 22pp; English.
XX	
CC	The patent discloses Streptomyces fradiae S-adenosylmethionine (SAM)
CC	operon which comprises three genes encoding SAM synthetase, methyl-
CC	transferase (MT) and methylene tetrahydrofolate reductase (MTHF).
CC	SAM synthetase, MT and MTHF together comprise the activated methyl
CC	cycle, which produces SAM and provides methyl groups required for
CC	the final steps in lysosin production. The invention also relates
CC	to vectors and transformed heterologous host cells for expressing
CC	SAM synthetase. It also relates to a method useful for producing
CC	operon from Streptomyces fradiae.
XX	
SQ	Sequence 4848 BP; 648 A; 1869 C; 1696 G; 635 U; 0 other;
OY	
Db	Query Match 17.0%; Score 40; DB 24; Length 4848; Best Local Similarity 40.4%; Pred. No. 0.0032; Matches 44; Conservative 8; Mismatches 57; Indels 0; Gaps 0;
OY	113 ACGTCAGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNACGGTTCATCAGA 172 ::
Db	2055 ACCUCCGCGCGGCCGGAUCACGCGAUCUGACCUCGCCGCCGAUCUCCGCACAGA 2114 :: :: :: :: :: :: :: :: ::
OY	173 CGCGGCATACGCGCACTTTGGCCGTGACGACGCGCACTTCACGCGCA 221 :: :: :: :: :: :: :: ::
Db	2115 CGCGCGCUACGCGCACUCUCCGCCGCAACUGCCGAGUUCACUCCGGA 2163 :: :: :: :: :: :: :: ::
RESULT 24	
AAAT5637/c	
ID	AAA75637 standard; DNA; 1693 BP.
XX	
AC-	AAA75637;
XX	
DT	22-JAN-2001 (first entry)
XX	
Nucleotide sequence of ORF15 encoding S-adenosylmethionine synthetase.	
XX	
Narbanolide synthase; polyketide synthase gene; narbanolide polyketide;	
KW	antibiotic; C12-hydroxylase; pick; desosamine biosynthesis;
KV	desomanglyl transferase enzyme; ketolide; beta-glucosidase enzyme;
KW	picromycin biosynthesis; ss.
OS	Streptomyces venezuelae.
PN	US6117659-A.
XX	
PD	12-SEP-2000.
XX	
PF	27-MAY-1999; 99US-0320878.
PR	
PR	28-MAY-1998; 98US-0087080.
PR	22-SEP-1998; 98US-0100880.
PR	08-FEB-1999; 99US-0119139.
PR	20-MAY-1999; 99US-0134990.
PR	30-APR-1997; 97US-0846247.
PR	06-MAY-1998; 98US-0073538.
PR	28-AUG-1998; 98US-0141908.
PA	(KOSA-) KOSAN BIOSCIENCES INC.
PI	Ashley G, Belach MC, Belach M, Tang L, McDaniel R;
DR	WPI: 2000-610844/58.
PT	New recombinant pick hydroxylase gene of Streptomyces venezuelae useful
PT	for converting ketolides to antibiotics and as antibiotics and
PT	intermediates in the synthesis of compounds with pharmaceutical value
XX	
XX	Disclosure; Columns 45-46; 117pp; English.

PI	Frazer CM, Hickey E, Peterson J, Tettein H, Venter JC;
PI	Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI	Rappuoli R, Pizza M.
XX	
DR	WPI: 2000-318079/27.
XX	
PT	Isolated nucleotide sequences of Neisseria meningitidis which can be
PT	used in the diagnosis and treatment of N. meningitidis infection and
PT	other Neisserial infections, for example, N.gonorrhoea .
XX	
PS	Claim 7: Page 507-524; 1760pp: English.
XX	
CC	The present invention describes methods of obtaining immunogenic
CC	proteins from Neisseria genomic sequences. AAA81453 to AAA82414
CC	represent specifically claimed Neisseria meningitidis genomic DNA
CC	sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
CC	Neisseria DNA sequences and their corresponding proteins; AAA81254 to
CC	AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
CC	isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
CC	AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC	sequences, which are all used in the exemplification of the present
CC	invention. The nucleic acid sequences, protein sequences, and antibodies
CC	against them, can be used in the manufacture of a composition. The
CC	composition can be used as a medicament (or in the manufacture of a
CC	medicament) for treating, preventing or diagnosing infection due to
CC	Neisserial bacteria. For example, some of the identified proteins could
CC	be components of vaccines against Meningococcus B; against all serotypes;
CC	and/or against all pathogenic Neisseriae. Identification of sequences
CC	from the bacterium will also facilitate production of biological probes,
CC	particularly organism-specific probes. Attempts to make efficacious
CC	Meningococcus B vaccines have failed mainly due to antigen tolerance.
CC	Multivalent vaccines have also been tried but none have successfully
CC	overcome antigenic variability. The provision of further, complete
CC	sequences may provide an opportunity to identify secreted or surface
CC	exposed proteins that may be presumed targets for the immune system and
CC	which are not antigenically variable or at least more conserved than
CC	other more variable regions.
XX	
SQ	Sequence 56485 BP: 12504 A; 14247 C; 16158 G; 13573 T; 3 other:
Query Match	14.7%; Score 34.6; DB 21; Length 56485;
Best Local Similarity	44.5%; Pred. No. 0.67; Mismatches 61; Indels 0; Gaps 0;
Matches 49; Conservative	0; Mismatches 61; Indels 0; Gaps 0;
OY	113 ACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNACAGTTCATCAGA 172
	I I
Db	54015 ACCCTGGCCCCCAAGACATGCACAAATGCTCATCTCTTGCGGCCGATTACGAATA 54074
	I I
OY	173 CGCGCGATTACGGCACATTGTGGCCGTGACGAGCCGCGACTTCACCTCGCGAC 222
	I I
Db	54075 CGCGCGATTACGACATTTCGGCCCGCGAAGACCTGACTTCATTGGGAG 54124
	I I
RESULT 28	
AAF21612/C	
ID	AAF21612 standard; DNA: 349980 BP.
XX	
AC	AAF21612:
XX	
DT	13-MAR-2001 (first entry)
DE	Neisseria meningitidis B nucleotide sequence SEQ ID NO:113.
XX	
KW	Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
ds.	diagnosis; antigen; detection; infection; gene therapy; antibacterial;
OS	Neisseria meningitidis.
PV	WO200066791-A1.
XX	
PN	09-NOV-2000.
DD	
XX	

[illegible]

XX	PN	WO200022430-A2.
XX	PD	20-APR-2000.
XX	PF	08-OCT-1999; 99WO-US23573.
XX	PR	09-OCT-1998; 98US-0103794.
XX	PR	30-APR-1999; 99US-0132068.
XX	PA	(CHIR) CHIRON CORP.
XX	PI	Frazier CM, Hickey E, Peterson J, Tetteijn H, Venter JC;
XX	PI	Masigiani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
XX	PI	Rappuoli R, Pizza M;
XX	DR	WPI: 2000-318079/27.
XX	PT	Isolated nucleotide sequences of Neisseria meningitidis which can be
XX	PT	used in the diagnosis and treatment of N. meningitidis infection and
XX	PT	other Neisserial infections, for example, N.gonorrhoea
XX	PS	Claim 7; Page 629-865; 1760pp; English.
XX	CC	The present invention describes methods of obtaining immunogenic
XX	CC	proteins from Neisseria genomic sequences. AAA81453 to AAA82414
XX	CC	represent specifically claimed Neisseria meningitidis genomic DNA
XX	CC	sequences: AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
XX	CC	Neisseria DNA sequences and their corresponding proteins: AAA81254 to
XX	CC	AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
XX	CC	isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
XX	CC	AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
XX	CC	sequences, which are all used in the exemplification of the present
XX	CC	invention. The nucleic acid sequences, protein sequences, and antibodies
XX	CC	against them, can be used in the manufacture of a composition. The
XX	CC	composition can be used as a medicament (or in the manufacture of a
XX	CC	medicament) for treating, preventing or diagnosing infection due to
XX	CC	Neisserial bacteria. For example, some of the identified proteins could
XX	CC	be components of vaccines against Meningococcus B; against all serotypes;
XX	CC	and/or against all pathogenic Neisseriae. Identification of sequences
XX	CC	from the bacterium will also facilitate production of biological probes,
XX	CC	particularly organism-specific probes. Attempts to make efficacious
XX	CC	Meningococcus B vaccines have failed mainly due to antigen tolerance.
XX	CC	Multivalent vaccines have also been tried but none have successfully
XX	CC	overcome antigenic variability. The provision of further, complete
XX	CC	sequences may provide an opportunity to identify secreted or surface
XX	CC	exposed proteins that may be presumed targets for the immune system and
XX	CC	which are not antigenically variable or at least more conserved than
XX	CC	other more variable regions.
XX	SO	Sequence 837096 BP; 207534 A; 227065 C; 205215 G; 197280 T; 2 other:
XX	QY	Query Match 14.7%; Score 34.6; DB 21; Length 837096;
XX	QY	Best Local Similarity 44.5%; Pred. No. 2.1;
XX	QY	Matches 49; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
XX	QY	113 ACGTCAGCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAAGCTCATCAGA 172
XX	QY	Db 452410 ACCTCGGCCCCCAAGAGCATCGTCCAAATGCTCGATCTCTTGCGCCGCGATTACAGTAAT 452351
XX	QY	173 CCGCGCATACGAGCCACTTTGGCCGTGACGACGCGCATCTTCACCTGCGAG 222
XX	QY	
XX	Db	452350 CCGCGCGTTAGGACATTTGGCGCGCAAGACCTGAGTTCACTTGGGAG 452301
XX	RESULT	30
XX	ID	AA199683 standard; DNA: 4403765 BP.
XX	AC	AA199683;
XX	XX	AA199683;
XX	DT	15-JAN-2002 (first entry)
XX	XX	

XX	24-JUN-1998;	980S-0103840.
PR	(GENO-) INST GENOMIC RES.	
PA	Fleischmann RD, White OR, Fraser CM, Venter JC:	
XX		
PI	WPT: 2001-647261/74.	
DR		
XX	Evaluating strain variation of Mycobacterium tuberculosis, comprises	
PT	determining the nucleotide sequence of the strain at positions in the	
PR	genome corresponding to positions where M. tuberculosis strains CDC	
PT	1551 and H37Rv differ -	
XX		
PS	Claim 3; SEQ ID NO 1; 3bp + Sequence Listing: English.	
CC	The invention relates to evaluating strain variation within and between	
CC	different populations of the tuberculosis bacterial pathogen,	
CC	Mycobacterium tuberculosis or related Mycobacterium by determining the	
CC	nucleotide sequence of the first strain at positions in the complete	
CC	sequence of the genome that correspond to positions that differ in the	
CC	nucleotide sequences of M. tuberculosis strains CDC 1551 (A1193683) and	
CC	H37Rv (A1193682). The method is useful for evaluating strain variation of	
CC	M. tuberculosis and has valuable application in the fields of	
CC	tuberculosis genetics, epidemiology, patient treatment and epidemic	
CC	monitoring.	
CC	Note: The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from USFTO	
CC	at seqdata.uspto.gov/sequence.html?DocID=6294328B1.	
SQ	Sequence 4411529 BP; 758565 A; 1449983 C; 144602 G; 758379 T; 0 Other:	
XX		
Query Match	14.6%; Score 34.4; DB 22; Length 4411529;	
Best Local Similarity	73.3%; Pred. No. 5.1;	
Matches	44; Conservative 0; Mismatches 16; Indels 0; Gaps 0;	
OY	171 GACCGCCGATAGCGCCTTGGCCGTGACGACGCCGACTTCACCTCGAGGTGCCTCA 230	
D5	1567944 GACC GCCGCGCTACGCGGACCTTGCGGCCGACCGAGCTGAATTACCGTGGGAGCAGCTCGA 1568003	
RESULT 32		
ABL09034/C		
ID	ABL09034 standard; cDNA; 17512 BP.	
XX		
AC	ABL09034;	
XX		
DT	26-MAR-2002 (first entry)	
XX		
DE	Drosophila melanogaster expressed polynucleotide SEQ ID NO 21584.	
XX		
KM	Drosophila; developmental biology; cell signalling; insecticide;	
KW	Pharmaceutical; gene; ss.	
XX		
OS	Drosophila melanogaster.	
XX		
PN	WO200171042-A2.	
XX		
PD	27-SEP-2001.	
XX		
PE	23-MAR-2001; 2001WO-US09231.	
XX		
PR	23-MAR-2000; 2000US-191637P.	
PR	11-JUL-2000; 2000US-0614150.	
XX		
PA	(PEKE) PE CORP NY.	
XX		
PI	Venter JC, Adams M, Li PWD, Myers EW;	
XX		
DR	WPT: 2001-656860/75.	
XX	P-PSDB; ABB64931.	
PT	New isolated nucleic acid detection reagent for detecting 1000 or more	

XX	Aspergillus oryzae EST SEQ ID NO:4949.
DE	
XX	
KW	Multiple gene expression; filamentous fungal cell; EST;
KM	expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KV	Aspergillus oryzae; Trichoderma reesei; identification; recombinantion;
KW	culture condition; environmental stress; spore morphogenesis;
KX	metabolic pathway engineering; catabolic pathway engineering; ss.
XX	
OS	Aspergillus oryzae.
PN	
PN	WO200056762-A2.
PD	
PD	28-SEP-2000.
XX	
XX	22-MAR-2000; 2000WO-US07781.
PR	
PR	22-MAR-1999; 99US-0273623.
PA	
PA	(NOVO) NOVO NORDISK BIOTECH INC.
PA	(NOVO) NOVO NORDISK AS.
XI	
XI	Berka RM, Rey MM, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
DR	
DR	WPI; 2000-594572/56.
PT	
PT	Monitoring differential expression of genes in filamentous fungal cells
PS	uses fluorescence-labeled nucleic acids isolated from the cells and a
XX	substrate of expressed sequence tags -
PS	
XX	Claim 88; Page 2084; 3161pp; English.
CC	
CC	The present invention describes a method for monitoring differential
CC	expression of genes in a first filamentous fungal (FF) cell relative to
CC	expression of the same genes in one or more second filamentous fungal
CC	cells. The method uses fluorescence-labeled nucleic acids isolated from
CC	the FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC	are used in the methods for monitoring differential expression of genes
CC	in a first filamentous fungal (FF) cell relative to expression of genes
CC	same genes in one or more second filamentous fungal cells. Monitoring
CC	the global expression of genes from FF cells allows the production
CC	potential of the microorganisms to be improved. New genes may be
CC	discovered, possible functions of unknown open reading frames can be
CC	identified and gene copy number variation and stability can be
CC	monitored. The expression of genes can be used to study how FF cells
CC	adapt to changes in culture conditions, environmental stress, spore
CC	morphogenesis, recombination, metabolic or catabolic pathway
CC	engineering. Using ESTs provides several advantages over genomic or
CC	random cDNA clones including elimination of redundancy as one spot on an
CC	array equals one gene or open reading frame, and organisation of the
CC	microarrays based on function of the gene products to facilitate
CC	analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC	Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
CC	niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
CC	AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
XX	all specifically claimed in the present invention.
XX	
SQ	Sequence 657 BP; 155 A; 175 C; 134 G; 193 T; 0 other;
Query Match	13.0%; Score 30.6; DB 21; Length 657;
Best Local Similarity	41.8%; Pred. No. 2, 3;
Matches	51; Conservative 0; Mismatches 71; Indels 0; Gaps 0
OY	113 ACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAGA 172
Dd	174 ACCTGATTTCCTGGCTGCACGTTGCCGCCCCGGAAGAAGCGAGCATCATGCGCATTGAGC 233
OY	173 CCGCCGCATACGCGCACACTTGGCCCGGTGACGACGCCGCACTTCACCTCGAGAGTGCACAAC 232
Dd	234 ACGCGAATTGGTCGAGTTGCTTATGACTACGTCGAGATTACCACCGCAGCTATCATGTG 293

```
DB      294 CC 295

RESULT 37
ABL29661
ID      ABL29661 standard; DNA: 2247 BP.
XX
AC      ABL29661;
XX
DT      26-MAR-2002 (first entry)
XX
DE      Drosophila melanogaster genomic polynucleotide SEQ ID NO 40456.
XX
KW      Drosophila; developmental biology; cell signalling; insecticide;
KW      pharmaceutical; gene; ds.
XX
OS      Drosophila melanogaster.
XX
PN      WO200171042-A2.
XX
PD      27-SEP-2001.
XX
PF      23-MAR-2001; 2001WO-US09231.
XX
PR      23-MAR-2000; 2000US-191637P.
PR      11-JUL-2000; 2000US-061415O.
PA      (PEKE ) PE CORP NY.
XX
PI      Venter JC, Adams M, Li PWD, Myers EW;
XX
DR      WPT: 2001-656860/75.
XX
PT      New isolated nucleic acid detection reagent for detecting 1000 or more
PR      genes from Drosophila and for elucidating cell signalling and cell-cell
PT      interactions -
XX
PS      Claim 1; SEQ ID NO 40456; 21pp + Sequence Listing; English.
CC
CC      The invention relates to an isolated nucleic acid detection reagent
CC      capable of detecting 1000 or more genes from Drosophila. The invention is
CC      useful in developmental biology and in elucidating cell signalling and
CC      cell-cell interactions in higher eukaryotes for the development of
CC      insecticides, therapeutics and pharmaceutical drugs. The invention
CC      discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC      sequences (ABL01840-ABL16175) and the encoded proteins
CC      (ABB57737-ABB72072).
CC      The sequence data for this patent did not form part of the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pct_sequences.
XX
SO      Sequence 2247 BP: 733 A; 488 C; 463 G; 563 T; 0 other:

Query Match          13.0%; Score 30.6; DB 23; Length 2247;
Best Local Similarity 41.8%; Pred. No. 4;
Matches    51; Conservative   0; Mismatches    71; Indels     0; Gaps       0;

OY      95 AATTGAGCAGCACACAACACTGTCTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 154
        ||||| I | I || I ||
DB      924 AATTCAGCGATTAAAGCATGGTTCAAAAAGACGGCGGAACAATTGCCATCGAGTAIG 983
OY      155 NNNNCAGGTTTCATCAGAAGCCGCATACGGCCACTTTTGCCGTACACAGCCGACTTCA 214
        || ||||||| ||||| ||| I | I | I | || || || || || || || || || ||
DB      984 GCATCAAGTTCATGAGACCTCCGCGAAGGCCAGCATTAACGTGAAGAAGCTTCTCCA 1043
OY      215 CC 216
        || ||
DB      1044 CC 1045
```


[illegible]

Db 85 CCGTGGCTGCGCCGCCGTTTTCATCAAGCCCCCGCCTACTGTGTACGTAAACATGCGGGGTAC 144

Oy 184 GGCCACTTTTGCCGCGTAGCAGCGGCAGATTTCACCTTCGAGAGTGTTGTAACCC 233
||||| ||||| | ||||| ||| | |||||
Db 145 CGCCAGATGGCGCTCAAAATACGACGATCTCCTCGAGGAGAGAACGAGAC 194

RESULT 39
AAV64373
ID AAV64373 standard; cDNA; 1519 BP.
XX
AC AAV64373;
DT 15-FEB-1999 (first entry)
XX
DE GABA-gated chloride channel TBW-a3 cDNA.
XX
KM TBW-a3; GABA-gated chloride channel; tobacco budworm; insecticide;
KM SS.
XX
OS Heliothis virescens.
XX
PH Key Location/Qualifiers
FH CDS 1..1446
FT /*tag= a
FT sig_peptide 1..66
FT /*tag= b
FT sig_peptide 67..1443
FT /*tag= c
XX
XX MO9849185-A1.
XX
XX PD 05-NOV-1998.
XX
PF 27-APR-1998; 98WO-US08563.
XX
PR 02-JAN-1998; 98US-0002361.
PR 28-APR-1997; 97US-0044976.
XX
PA (FMCC) FMC CORP.
XX
PI Halling BP, Yuhas DA;
XX
DR WPI: 1999-009411/01.
DR P-PSDB; AAM81635-36.
XX
XX
PT New isolated lepidoptera GABA-gated chloride channels - comprise 3
PT isoforms isolated from the tobacco budworm *Heliothis virescens*, used
PT for characterizing bioactive agents, e.g. insecticides
XX
PS Claim Id: Fig 2; 55pp; English.
XX
CC This cDNA sequence encompasses the open reading frame encoding
CC GABA-gated chloride channel TBW-a3 (see AAM81635-36) of tobacco
CC budworm (*Heliothis virescens*). TBW-a3, TBW-a2 (see AAM81633-34)
CC and TBW-a1 (see AAM81637) proteins are 3 receptor isoforms that show
CC sequence homology to each other and to other insect GABA-gated
CC chloride channels. TBW-2a cDNA was obtained from *H. virescens* 4th
CC instar larva RNA by PCR and RACE amplifications. The invention
CC provides expression vectors in which a nucleic acid encoding a
CC GABA-gated chloride channel is driven by an inducible promoter, and
CC a claimed process for producing a GABA-gated chloride channel by
CC transformed cells. The GABA-gated channels or cells expressing
CC them can be used for characterizing a bioactive agent (claimed).
CC e.g. for use as an insecticide. Probes and primers that identify
CC or amplify GABA-gated chloride channel nucleic acids of the
CC invention are also claimed.
XX
SQ Sequence 1519 BP; 421 A; 362 C; 347 G; 388 T; 1 other;

Query Match 12.7%; Score 29.8; DB 20; Length 1519;
Best Local Similarity 40.5%; Pred. No. 6.3;
Matches 64; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

RESULT 41
AAT86246/c
ID AAT86246 standard; cDNA to mRNA, 1683 BP.

OY	142	NNNNNNNNNNNNNNNNNNN	CAGGTTTCATCAAGCCGCCCATCAGGCACATTGGCGGTGAC	201
		" "	" "	" "
Db	2167	TACTTCAACATTAAATCAGCTTTTGCCAAGGCTTGGGAGCGACACTACAAGAAGCACAGAT	2227	
OY	202	GACGCCGACTTTCACCTGCGGAGTGG	226	
		" "	" "	" "
Db	2227	ATCATGGGCTGCCCTGCTGGCTGG	2251	

RESULT 41
AA186246/C
ID AA186246 standard; cDNA to mRNA; 1683 BP.
XX
AC AA186246;
XX
DT 07-JAN-1998 (first entry)
XX

KW Cofactor-independent phosphoglycerate mutase; PGM-1; E.C. 5.4.2.1.

KW T cell; epitope; immunotherapy; detection; diagnosis; hay fever;

XX
XX

FH	Key	Location
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

ET

PN W09705258-A2

PD 13-FEB-1997.

PF 02-AUG-1996; 96MO-AT00141.
XY

PR 02-AUG-1995; 95AT-0001320.
XX

(FROM / FROM FIVE & UNDECEAS GMDH.
XX
XX

Kraft D, Richter K, Rheinberger H;

DR WPI; 1997-145695/13

XX

PT antigenic epitope(s) - useful for diagnosis or treatment of

XX

[illegible]

CC mutase (PGM-1) isoform Art17. PGM-1 is a highly conserved plant allergen (analogue) which can cause cross-reactivity in patients allergic to

CC pollen and plant-derived foods. PGM-1 and its B cell and T cell epitopes can be used for the *in vitro* detection of allergy against CC.

PGM-1, by measuring serum IgE or a cellular reaction. They can also be used in immunotherapy and will not cause an autoimmune response because

CC PGM-1 is significantly different from the human enzyme, which is
CC co-factor dependent

Sequence 1683 bp: 466 A: 304 C: 456 G: 457 T: 0 other: 0

Query Match	12.5%	Score 29.4	DB 18	Length 1683
-------------	-------	------------	-------	-------------

```

Best Local Similarity 40.58, Fied. NO. 5.1,
Matches 54; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

```

QY 98 TGAGCAGGACACAACACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 157

Db 1421 TGATCCGAGTCACCACATATATTCACCTACTTCCTTATTCATCAAGATCATCTTA 1362

Sequence 2604 BP; 779 A; 515 C; 579 G; 731 T; 0 other;

Query Match 12.4%; Score 29; 2; DB 21; Length 2604;
Best Local Similarity 75.8%; Pred. No. 13;
Matches 50; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

38 CCATGCTGATTAATGACGCTCTGATTCATGTTGTTGTTATTAATGTAAT 97
|||||
DB 2330 CCATGCTGATTAATGATGGCTCTGTTCCCTTT---TGTTTATTAATGTTGTAAT 2386

OY 98 TGAGCA 103
|||||
DB 2387 TGAGCA 2392

RESULT 44
ABL04431/C
ID ABL04431 standard; cDNA: 1086 BP.

AC ABL04431;
XX
XX 26-MAR-2002 (first entry)

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7775.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EW;

DR WPI; 2001-656660/75.

P-PSDB; ABB60328.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -

PS Claim 1; SEQ ID NO 7775; 21bp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (AB101840-ABL16175) and the encoded proteins
XX (AB57737-AB872072).

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pub/published_pct_sequences.

XX Sequence 1086 BP; 295 A; 267 C; 273 G; 251 T; 0 other;

Query Match 12.3%; Score 29; DB 23; Length 1086;
Best Local Similarity 40.0%; Pred. No. 10;
Matches 68; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

OY 36 GCCATGCTGATTAATGACGCTCTGATTCATGTTGTTATTAATGTTGATA 95
|||||
DB 943 GCCATATCCGTAAGGAGGTCCTCGTAGACGCTATTCGGCTAGCTATAA 884

OY 96 ATTGACAGACACACACAGTACTTNNNNNNNNNNNNNNNNNNNNNNNNNNNN 155
|||||
DB 883 ATTGATTCAGACACCCCTGCCACACCAAGCATCAGGGGCTACCGAATCCAGTCGG 824

OY 156 NNNCAGGTTGATCAAGACCGCCGATACGACCTTTGGCCGTGACGAG 205
|||||
DB 823 TCTCGTGCCATCCCATCCATGCGACATCATGATGATGCTCTTATGACG 774

RESULT 45
AAH66738
ID AAH66738 standard; DNA: 1221 BP.

AC AAH66738;

DT 26-SEP-2001 (first entry)

XX C glutamicum coding sequence fragment SEQ ID NO: 1773.

DE Corynebacterium; amino acid synthesis; vitamin; saccharide;

KW organic acid synthesis; ds.

XX Corynebacterium glutamicum.

XX EP1108790-A2.

PD 20-JUN-2001.

PF 18-DEC-2000; 2000EP-0127688.

XX 16-DEC-1999; 99JP-0377484.

PR 07-APR-2000; 2000JP-0159162.

PR 03-AUG-2000; 2000JP-0280988.

XX (KIOW) KIOWA HAKKO KOGYO KK.

XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

DR WPI; 2001-376931/40.

P-PSDB; AAG91519.

PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying
XX mutation point of a gene, measuring expression of a gene, analysing
XX expression profile or pattern of a gene and identifying homologous gene
XX -

PS Claim 8; SEQ ID NO: 1773; 246bp + Sequence Listing; English.

XX The present invention provides a number of nucleotide and protein
XX sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These
XX are useful for identifying the mutation point of a gene derived from a
XX mutant of corynebacterium bacterium, measuring expression amount and
XX analysing the expression profile or expression pattern of a gene derived
XX from Corynebacterium bacterium, and identifying a homologue of a gene derived
XX from Corynebacterium bacterium. Corynebacterium bacteria are useful for producing
XX amino acids, nucleic acids, vitamins, saccharides and organic acids,
XX particularly L-lysine. The present sequence is a nucleic acid described
XX in the exemplification of the invention.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.

XX Sequence 1221 BP; 272 A; 350 C; 336 G; 263 T; 0 other;

Query Match 12.3%; Score 29; DB 22; Length 1221;
Best Local Similarity 41.0%; Pred. No. 11;
Matches 50; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

OY 113 ACGTCAGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 172
|||||
DB 1067 ACGTCGTCAGACACCAATATCCGTGATCTGCTTCGATCGATCTACGCTACA 1126

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 23, 2003, 12:06:28 : Search time 19.5833 Seconds
(without alignments)
2307.226 Million cell updates/sec

Title: US-09-198-779b-1

Perfect score: 349
Sequence: 1 gtttcgcgtctagctcgtt.....ctgcgagtggtgcaagccccc 235

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Command line parameters:
-MODEL=Frame+ n2p.model -DEV=xip
-O=/cgn2.1/USPTO.spool/US09198779/runat.23042003.120617.2416/app.query.fasta.1.917
-DB=PIR.73 -OPMT=fastan -SUFFIX=rrr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=DIOSUM62 -TRANS=human40.cdi -LIST=50
-DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE=LOCAL
-OUTFM=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09198779.qcgn.1.1.92@unat.23042003.120617.2416 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: PIR.73:*

1: pir1:*\n2: pir2:*\n3: pir3:*\n4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	127	36.4	394	2 T06180 methionine adenosyl
2	120	34.4	68	2 PQ0817 methionine adenosyl
3	120	34.4	393	2 JN0131 methionine adenosyl
4	120	34.4	393	2 S38875 methionine adenosyl
5	120	34.4	393	2 S46538 methionine adenosyl
6	120	34.4	393	2 S46538 methionine adenosyl
7	116	33.2	360	2 T06582 methionine adenosyl
8	116	33.2	366	2 S66351 methionine adenosyl
9	115	33.0	390	2 G84785 probable s-adenosyl
10	115	33.0	393	2 J00410 methionine adenosyl
11	108.5	31.1	397	2 S66352 methionine adenosyl
12	101	28.9	179	2 T07899 methionine adenosyl
13	101	28.9	390	2 S49491 methionine adenosyl
14	101	28.9	390	2 S46540 methionine adenosyl

15	98	28.1	396	2 T10710 methionine adenosyl
16	74	21.2	395	2 G72228 S-adenosylmethionin
17	72	20.6	389	2 E81986 probable methionin
18	72	20.6	388	2 D81042 S-adenosylmethionin
19	68	19.5	388	2 S51671 methionine adenosyl
20	65	18.6	400	2 D69657 methionine adenosyl
21	64.5	18.5	407	2 B87255 S-adenosylmethionin
22	64	18.3	376	2 A82895 S-adenosylmethionin
23	63.5	18.4	1979	2 J00059 mtrpD protein - mo
24	63	18.1	395	1 S27257 methionine adenosyl
25	63	18.1	395	2 A37118 methionine adenosyl
26	63	18.1	403	2 H86976 probable S-adenosyl
27	63	18.1	589	2 G87485 hypothetical prote
28	61	17.5	376	2 F90589 S-adenosylmethionin
29	61	17.5	385	2 D71964 S-adenosylmethionin
30	61	17.5	385	2 E64544 methionine adenosyl
31	61	17.5	398	2 F89664 S-adenosylmethionin
32	61	17.5	399	2 D84062 S-adenosylmethionin
33	61	17.5	399	2 F86862 methionine adenosyl
34	61	17.5	399	2 AD1654 S-methionine adeno
35	61	17.5	399	2 AH1282 S-methionine adeno
36	61	17.5	403	2 F70899 probable metk prot
37	61	17.5	420	2 B97403 methionine adenosyl
38	61	17.5	420	2 AB2621 S-adenosylmethionin
39	61	17.5	877	2 AC2211 heme transport pro
40	60.5	17.3	409	2 S74736 methionine adenosyl
41	60	17.2	385	2 E82319 S-adenosylmethionin
42	60	17.3	674	2 B84381 acylaminoacyl-pept
43	59	16.9	396	2 A71281 probable S-adenosyl
44	59	16.9	396	2 A47151 methionine adenosyl
45	59	16.9	397	2 H89787 hypothetical prote
46	58.5	16.9	155	2 H70866 hypothetical prote
47	58.5	16.8	238	2 E84977 methionine adenosyl
48	58	16.6	472	2 G75298 ribosomal protein
49	58	16.6	472	2 G75298 microtubule-associ
50	58	16.6	1861	2 T13845

ALIGNMENTS

RESULT 1
T06180
methionine adenosyltransferase (EC 2.5.1.6) - barley
N:Alternate names: S-adenosylmethionine synthetase
C:Species: Hordeum vulgare (barley)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Jun-2000
C:Accession: T06180
R:Mori, S.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z15512
A:Accession: T06180
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-394 <MOR>
A:Cross-references: EMBL:D63835; PIDD:BAA09895.1
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.: 2.4e-10
Score: 127.00
Percent Similarity: 96.00%
Best Local Similarity: 96.00%
Query Match: 36.39%
DB: 2
Gaps: 0

US-09-198-779b-1 (1-235) x T06180 (1-394)

OY AGGTTTCATCAGACCGCCGATACGGCCATTGGCCGTGACGACCGCCACTTCACCTGC 219
|||||
Db 362 ArghpellellysthrAlaAlaIatYcIylhisPhcglYatgAspAlaAspPheThrTrp 381
OY 220 GAGGTGTCACAGCCC 234

Db 382 GluValVallyspro 386

RESULT 2

P00817

methionine adenosyltransferase (EC 2.5.1.6) - rape (fragment)

C:Species: Brassica napus (rape)

C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 05-May-2000

C:Accession: P00817

R:Park, Y.S.; Kwak, J.M.; Kwon, O.Y.; Kim, Y.S.; Lee, D.S.; Cho, M.J.; Lee, H.H.; Nam, H.

Plant Physiol. 103, 359-370, 1993

A:Title: Generation of expressed sequence tags of random root cDNA clones of Brassica na

A:Reference number: P00816; MWID:94302145; PMID:8029352

A:Accession: P00817

A:Molecule type: mRNA

A:Residues: 1-68 <PAR>

A:Experimental source: root, cv. Naehan

C:Superfamily: methionine adenosyltransferase

C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	2,54e-09	Length:	68
Score:	120.00	Matches:	22
Percent Similarity:	92.00%	Conservative:	1
Best Local Similarity:	88.00%	Mismatches:	2
Query Match:	34.38%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x P00817 (1-68)

QY 160 AGGTTTCATCAAGACCGCGCATAGCGCACTTTGGCCGTGACGACGCCGCACTTACCTGC 219

Db 36 ArgPheLeuysThrAlaAlaTyGlyHisPheGlyArgAspAspProAspPheThrTrp 55

QY 220 GAGGTGTCACAGCCC 234

Db 56 GluValVallyspro 60

RESULT 3

JN0131

methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana

N:Alternate names: S-adenosylmethionine synthetase

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-May-2000

C:Accession: JN0131

R:Peleman, J.; Boerjan, W.; Engler, G.; Seurinck, J.; Botterman, J.; Alliotte, T.; Van M

Plant Cell 1, 81-93, 1989

A:Title: Strong cellular preference in the expression of a housekeeping gene of Arabidop

A:Reference number: JN0131; MWID:92386056; PMID:2535470

A:Accession: JN0131

A:Molecule type: DNA

A:Residues: 1-393 <PEL>

A:Cross-references: GB:M50507; NID:q166871; PIDN:AAA32866.1; PID:q166872

A:Experimental source: var. K85

A:Note: the sequence derived from var. Columbia differs from that shown in having 117-Gl

C:Comment: S-Adenosylmethionine synthetase catalyzes the biosynthesis of adenosylmethio

C:Keywords: S-adenosylmethionine; transferase

A:Gene: sam-1

C:Superfamily: methionine adenosyltransferase

C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	2,76e-09	Length:	393
Score:	120.00	Matches:	22
Percent Similarity:	92.00%	Conservative:	1
Best Local Similarity:	88.00%	Mismatches:	2
Query Match:	34.38%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x JN0131 (1-393)

QY 160 AGGTTTCATCAAGACCGCGCATAGCGCACTTTGGCCGTGACGACGCCGCACTTACCTGC 219

Db 361 ArgPheLeuysThrAlaAlaTyGlyHisPheGlyArgAspAspProAspPheThrTrp 380

QY 220 GAGGTGTCACAGCCC 234

Db 381 GluValVallyspro 385

RESULT 4

S38875

methionine adenosyltransferase (EC 2.5.1.6) - tomato

N:Alternate names: S-adenosyl-L-methionine synthetase

C:Species: Lycopersicon esculentum (tomato)

C:Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000

C:Accession: S46539; S38875

R:Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.

Plant Mol. Biol. 25, 217-227, 1994

A:Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in

A:Reference number: S46538; MWID:94289646; PMID:8018871

A:Accession: S46539

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-393 <ES2>

A:Cross-references: EMBL:Z24742; NID:q429105; PIDN:CAA80866.1; PID:q429106

C:Superfamily: methionine adenosyltransferase

C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	2,76e-09	Length:	393
Score:	120.00	Matches:	22
Percent Similarity:	92.00%	Conservative:	1
Best Local Similarity:	88.00%	Mismatches:	2
Query Match:	34.38%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x S38875 (1-393)

QY 160 AGGTTTCATCAAGACCGCGCATAGCGCACTTTGGCCGTGACGACGCCGCACTTACCTGC 219

Db 361 ArgPheLeuysThrAlaAlaTyGlyHisPheGlyArgAspAspProAspPheThrTrp 380

QY 220 GAGGTGTCACAGCCC 234

Db 381 GluValVallyspro 385

RESULT 5

S46538

methionine adenosyltransferase (EC 2.5.1.6) - tomato

N:Alternate names: S-adenosyl-L-methionine synthetase

C:Species: Lycopersicon esculentum (tomato)

C:Date: 26-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000

C:Accession: S46538; S38874

R:Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.

Plant Mol. Biol. 25, 217-227, 1994

A:Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in

A:Reference number: S46538; MWID:94289646; PMID:8018871

A:Accession: S46538

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-393 <ESP>

A:Cross-references: EMBL:Z24741; NID:q429103; PIDN:CAA80865.1; PID:q429104

C:Superfamily: methionine adenosyltransferase

C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	2,76e-09	Length:	393
Score:	120.00	Matches:	22
Percent Similarity:	92.00%	Conservative:	1
Best Local Similarity:	88.00%	Mismatches:	2
Query Match:	34.38%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x S46538 (1-393)

methionine adenosyltransferase (EC 2.5.1.6) - garden petunia
 C:Species: Petunia x hybrida (garden petunia)
 C:Date: 01-Feb-1995 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
 C:Accession: S49491

R.Izhaki, A.; Shoseyov, O.; Weiss, D.
 submitted to the EMBL Data Library, October 1994
 A:Description: Petunia cDNA encoding S-Adenosylmethionine synthetase.
 A:Reference number: S49491

A:Accession: S49491
 A:Molecule type: mRNA
 A:Residues: 1-390 <I2H>
 A:Cross-references: EMBL:X82214; NID:g559505; PIDN:CA57696.1; PID:g559506
 C:Superfamily: methionine adenosyltransferase
 C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
 Pred. No.: 2.1e-06 Length: 390
 Score: 101.00 Matches: 19
 Percent Similarity: 83.33% Conservative: 1
 Best Local Similarity: 79.17% Mismatches: 4
 Query Match: 28.94% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779B-1 (1-235) x S49491 (1-390)

OY 160 AGGTTTCATCAGACCGCGCATACGCGCCTTGGCCGTGACGACGCCGACTTCACCTGC 219
 |||:|||||
 DB 361 ArgTYrGlnLysThrAlaIatYrGlnHspheGlyArgAspAspProAspPheThrTrp 380

OY 220 GAGGTGCTCAAG 231
 |||
 DB 381 GluThrValLys 384

RESULT 14

S46540
 methionine adenosyltransferase (EC 2.5.1.6) - tomato

N:Alternate names: S-adenosyl-L-methionine synthetase
 C:Species: Lycopersicon esculentum (tomato)

C:Date: 26-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
 C:Accession: S46540; S38876

R.Espartaco, J.; Plator-Toro, J.A.; Pardo, J.M.
 Plant Mol. Biol. 25, 217-227, 1994

A:Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in res
 A:Reference number: S46538; MUID:94289646; PMID:8018871

A:Accession: S46540
 A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
 A:Residues: 1-390 <ESP>

A:Cross-references: EMBL:Z24743; NID:g429107; PIDN:CA80867.1; PID:g429108
 C:Superfamily: methionine adenosyltransferase

C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
 Pred. No.: 2.1e-06 Length: 390
 Score: 101.00 Matches: 19
 Percent Similarity: 83.33% Conservative: 1
 Best Local Similarity: 79.17% Mismatches: 4
 Query Match: 28.94% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779B-1 (1-235) x S46540 (1-390)

OY 160 AGGTTTCATCAGACCGCGCATACGCGCCTTGGCCGTGACGACGCCGACTTCACCTGC 219
 |||:|||||
 DB 361 ArgTYrGlnLysThrAlaIatYrGlnHspheGlyArgAspAspProAspPheThrTrp 380

OY 220 GAGGTGCTCAAG 231
 |||
 DB 381 GluThrValLys 384

RESULT 15
 T10710
 methionine adenosyltransferase (EC 2.5.1.6) - clove pink

N:Alternate names: S-adenosylmethionine synthetase
 C:Species: Dianthus caryophyllus (clove pink)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-May-2000
 C:Accession: T10710

R.Larsen, P.B.; Woodson, W.R.
 submitted to the EMBL Data Library, April 1991

A:Description: Cloning and nucleotide sequence of a S-adenosylmethionine synthetase c
 A:Reference number: 217091

A:Accession: T10710
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-396 <LAR>
 A:Cross-references: EMBL:M61882; NID:g167961; PID:g304637
 C:Genetics: SAM2

C:Function: catalyzes the formation of S-adenosyl methionine with phosphate and py
 C:Superfamily: methionine adenosyltransferase
 C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
 Pred. No.: 5.98e-06 Length: 396
 Score: 98.00 Matches: 17
 Percent Similarity: 83.33% Conservative: 3
 Best Local Similarity: 70.83% Mismatches: 4
 Query Match: 28.08% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779B-1 (1-235) x T10710 (1-396)

OY 160 AGGTTTCATCAGACCGCGCATACGCGCCTTGGCCGTGACGACGCCGACTTCACCTGC 219
 |||:|||||
 DB 364 ArgTYrLeuLysThrAlaIatYrGlnHspheGlyArgGluAspProAspPheThrTrp 383

OY 220 GAGGTGCTCAAG 231
 |||
 DB 384 GluAlaIatLys 387

RESULT 16

G72228
 S-adenosylmethionine synthetase - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: G72228
 R.Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.

Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: G72228
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-395 <ARN>

A:Cross-references: GB:AE001807; GB:AE000512; NID:g4982216; PIDN:AA036725.1; PID:g498
 A:Experimental source: strain MSB8

C:Genetics: TML658
 C:Superfamily: methionine adenosyltransferase

Alignment Scores:
 Pred. No.: 0.026 Length: 395
 Score: 74.00 Matches: 13
 Percent Similarity: 88.89% Conservative: 3
 Best Local Similarity: 72.22% Mismatches: 2
 Query Match: 21.20% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779B-1 (1-235) x G72228 (1-395)

OY 169 AAGACCGCGCATACGCGCCTTGGCCGTGACGACGCCGACTTCACCTGCAG 222
 |||:|||||
 DB 364 LysThrAlaIatYrGlnHspheGlyArgAsnGluGluPheThrTrp 381

Best Local Similarity: 31.15% Mismatches: 27
Query Match: 18.05% Indels: 12
DB: 2 Gaps: 2

US-09-198-779B-1 (1-235) x G87485 (1-589)

QY 53 GACGGTCCTGATTCATGTTGTTGTTATTAATGATGACGACACAC 112
|||||
Db 240 AspGlyProAspPro-----GlnGlyProMet 248
|||||

QY 113 ACCTACCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGTTCTACAGA 172
|||||

Db 249 ThrIstGlnAlaArgAlaAnglySerSerSerAlaGlyAlaMetAlaSerSer--- 267
|||||

QY 173 CCGCCGATACGCGCCTTTGGCCGTCGACGCGCCTTACCTCGCAGGTCGTCACGC 232
|||||

Db 268 ProProAlaGlnSerAlaArgLeuAlaAlaAspAlaProAspAlaAlaIleThrSer 287
|||||

QY 233 CCC 235
|||

Db 288 Pro 288

RESULT 28

hypothetical protein MYPU_7020 [Imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: F90599
R:Chamaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Sanson, D.; Gallsson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; M0ID:21267165; PMID:11353084
A:Accession: F90599
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <KUR>
A:Cross-references: GB:AL445566; PID:g14090117; PIDN:CAC13875.1; GSPDB:GN00153
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU_7020
A:Genetic code: SGC3
C:Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.: 2.43 Length: 376
Score: 61.00 Matches: 10
Percent Similarity: 66.67% Conservative: 4
Best Local Similarity: 47.62% Mismatches: 7
Query Match: 17.48% Indels: 0
DB: 2 Gaps: 0

US-09-198-779B-1 (1-235) x F90599 (1-376)

QY 160 AGGTTCATCAAGACCGCCGATACGCGCCTTTGGCCGTGACACAGCGCCGACTTACCTGC 219
|||||

Db 343 LysTyrThrProThrSerPhePheGlyHisPheGlyArgAspSerLeuAspLeuProTrp 362
|||||

QY 220 GAG 222
|||

Db 363 Glu 363

RESULT 29

D71964
s-adenosylmethionine synthetase - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 18-Jun-1999
C:Accession: D71964
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Metberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; M0ID:99120557; PMID:9923682

A:Accession: D71964
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-385 <ARN>
A:Cross-references: GB:AE001456; GB:AE001439; MID:g4154689; PIDN:AAD05755.1; PID:g415
A:Experimental source: strain J99
C:Genetics:
A:Gene: metK
C:Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.: 2.43 Length: 385
Score: 61.00 Matches: 11
Percent Similarity: 82.35% Conservative: 3
Best Local Similarity: 64.71% Mismatches: 3
Query Match: 17.48% Indels: 0
DB: 2 Gaps: 0

US-09-198-779B-1 (1-235) x D71964 (1-385)

QY 172 ACCGCGCATACGCGCCTTTGGCCGTGACGACGCGCCTTACCTGCAG 222
|||||

Db 355 ThrSerAlaTyrGlyHisPheGlyArgGluLeuGluGluPheTrpGlu 371
|||||

RESULT 30

E64544
methionine adenosyltransferase (EC 2.5.1.6) 2 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 05-May-2000
C:Accession: E64544
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glöck, A.; McKe
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser,
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; M0ID:97394467; PMID:9252185
A:Accession: E64544
A>Status: preliminary
A:Molecule type: nucleic acid sequence not shown; translation not shown
A:Residues: 1-385 <TOM>
A:Cross-references: GB:AE000540; GB:AE000511; MID:g2313287; PIDN:AAD07267.1; PID:g231
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.: 2.43 Length: 385
Score: 61.00 Matches: 11
Percent Similarity: 82.35% Conservative: 3
Best Local Similarity: 64.71% Mismatches: 3
Query Match: 17.48% Indels: 0
DB: 2 Gaps: 0

US-09-198-779B-1 (1-235) x E64544 (1-385)

QY 172 ACCGCGCATACGCGCCTTTGGCCGTGACGACGCGCCTTACCTGCAG 222
|||||

Db 355 ThrSerAlaTyrGlyHisPheGlyArgGluLeuGluGluPheTrpGlu 371
|||||

RESULT 31

F89964
s-adenosylmethionine synthetase [Imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: F89964
R:Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsesu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; M0ID:21311952; PMID:11418146
A:Accession: F89964
A>Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-398 <RUR>
 A:Cross-references: GB:BA000018; PID:g13701583; PIDN:BA842876.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: metK
 C:Superfamily: methionine adenosyltransferase

Alignment Scores:
 Pred. No.: 2.43 Length: 398
 Score: 61.00 Matches: 11
 Percent Similarity: 72.22% Conservative: 2
 Best Local Similarity: 66.67% Mismatches: 5
 Query Match: 17.48% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779B-1 (1-235) x F89964 (1-398)

OY 169 AAGACCGCCGATACGCGCATTGGCCGTGACGACCGCGACTTCACCTCGGAG 222
 DB 367 GlnThrAlaIalrGlyrGlyHisPheGlyArgThrAspValGluLeuProTrpGlu 384

RESULT 32

S:adenosylmethionine synthetase metK [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence-revision 01-Dec-2000 #text-change 15-Jun-2001
 C:Accession: D84062
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
 Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: AB3650; MUID:20512582; PMID:11058132
 A:Accession: D84062
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-399 <STO>
 A:Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BA807019.1; GSPDB:GN00
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: metK
 C:Superfamily: methionine adenosyltransferase

Alignment Scores:
 Pred. No.: 2.43 Length: 399
 Score: 61.00 Matches: 11
 Percent Similarity: 72.22% Conservative: 2
 Best Local Similarity: 61.11% Mismatches: 5
 Query Match: 17.48% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779B-1 (1-235) x D84062 (1-399)

OY 169 AAGACCGCCGATACGCGCATTGGCCGTGACGACCGCGACTTCACCTCGGAG 222
 DB 370 GlnThrAlaIalrGlyrGlyHisPheGlyArgThrAspValGluLeuProTrpGlu 387

RESULT 33

F86862
 methionine adenosyltransferase (EC 2.5.1.6) [imported] - Lactococcus lactis subsp. lactis
 N:Alternate names: S-adenosylmethionine synthetase
 C:Species: Lactococcus lactis subsp. lactis
 C>Date: 23-Mar-2001 #sequence-revision 23-Mar-2001 #text-change 03-Aug-2001
 C:Accession: F86862
 R:Biolotin, A.; Wincker, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
 A:Reference number: AB6625; MUID:21235186; PMID:11337471
 A:Accession: F86862
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-399 <STO>
 A:Cross-references: GB:AE005176; PID:g12724937; PIDN:AAK06000.1; GSPDB:GN00146
 A:Experimental source: strain IL1403

C:Genetics:
 A:Gene: metK
 C:Superfamily: methionine adenosyltransferase
 C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
 Pred. No.: 2.43 Length: 399
 Score: 61.00 Matches: 11
 Percent Similarity: 72.22% Conservative: 2
 Best Local Similarity: 61.11% Mismatches: 5
 Query Match: 17.48% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779B-1 (1-235) x F86862 (1-399)

OY 169 AAGACCGCCGATACGCGCATTGGCCGTGACGACCGCGACTTCACCTCGGAG 222
 DB 368 GlnThrAlaIalrGlyrGlyHisPheGlyArgThrAspValGluLeuProTrpGlu 385

RESULT 34

AD1654
 S-methionine adenosyltransferase homolog metK [imported] - Listeria innocua (strain C
 C:Species: Listeria innocua
 C>Date: 27-Nov-2001 #sequence-revision 27-Nov-2001 #text-change 14-Dec-2001
 C:Accession: AD1654
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
 Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maltournam, A.;
 Ok, C.; Schlueter, T.; Sinoes, N.; Tilleret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
 A>Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AD1654
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-399 <GLA>
 A:Cross-references: GB:AL592022; PIDN:CA697004.1; PID:g16414260; GSPDB:GN00178
 A:Experimental source: strain C1P11262
 C:Genetics:
 A:Gene: metK
 C:Superfamily: methionine adenosyltransferase

Alignment Scores:
 Pred. No.: 2.43 Length: 399
 Score: 61.00 Matches: 11
 Percent Similarity: 72.22% Conservative: 2
 Best Local Similarity: 61.11% Mismatches: 5
 Query Match: 17.48% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779B-1 (1-235) x AD1654 (1-399)

OY 169 AAGACCGCCGATACGCGCATTGGCCGTGACGACCGCGACTTCACCTCGGAG 222
 DB 368 GlnThrAlaIalrGlyrGlyHisPheGlyArgSerAspLeuAspLeuProTrpGlu 385

RESULT 35

AH1282
 S-methionine adenosyltransferase homolog metK [imported] - Listeria monocytogenes (st
 C:Species: Listeria monocytogenes
 C>Date: 27-Nov-2001 #sequence-revision 27-Nov-2001 #text-change 14-Dec-2001
 C:Accession: AH1282
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
 Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maltournam, A.;
 Ok, C.; Schlueter, T.; Sinoes, N.; Tilleret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
 A>Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AH1282
 A:Status: preliminary

[illegible]

Db 367 ArgPheTYGlnAspValAlaAlaTyrGlnHisPheGlyAraGaaAspLeuAspLeuPro 386
 Oy 217 TGGCAG 222
 Db 387 TGTGln 388
 |||
 RESULT 41
 E82319
 S-adenosylmethionine synthase VC0472 [imported] - *Vibrio cholerae* (strain N16961 sero
 C:Species: *Vibrio cholerae*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: E82319
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.
 charlson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoli, I.; Sellers
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: E82319
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-385 <STO>
 A:Cross-references: GB:AE004133; GB:AE003852; NID:96654889; PIDN:AAF93645.1; GSPDB:GN
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 A:Gene: VC0472
 A:Map position: 1
 C:Superfamily: methionine adenosyltransferase

Alignment Scores:
 Pred. No.: 3 45 Length: 385
 Score: 60.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 83.33% Mismatches: 0
 Query Match: 17.19% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779B-1 (1-235) x E82319 (1-385)

Oy 169 AAGACCGCCGATAGCGCCACTTTGGCCGTGACGAC 204
 |||||||||||||||||||||||||||||||
 Db 355 LysThrAlaAlaTyrGlnHisPheGlyAraGlnGlu 366

RESULT 42
 B84381
 acylaminoacyl-peptidase [imported] - *Halobacterium* sp. NRC-1
 C:Species: *Halobacterium* sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: B84381
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky
 ; Leitthausner, B.; Keller, K.; Cruz, R.; Ganson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.;
 A:Title: Genome sequence of *Halobacterium* species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: B84381
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-674 <STO>
 A:Cross-references: GB:AE004437; NID:91058175; PIDN:AAG20414.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: yuxL

Alignment Scores:
 Pred. No.: 3 54 Length: 674
 Score: 60.00 Matches: 25
 Percent Similarity: 31.03% Conservative: 2
 Best Local Similarity: 28.74% Mismatches: 28
 Query Match: 17.34% Indels: 32
 DB: 2 Gaps: 3

US-09-198-779B-1 (1-235) x B84381 (1-674)

```

Oy 228 GACCACCTCGAGTGAAGTCGGCGCTCACGGCCAAAGTCGGCGTATGCGC----- 175
    ||| ||||| ||| ||||| ||||| ||||| |||||
Db 183 AspleuAlaAlaGlyArgValAspArgValThrAlaGlyValAlaGlySGLylyPro 202
Oy 174 -----GGTCTTGAT----- 166
Db 203 AlaTrpGlyAspAspGlyThrLeuTyTrProIleArgGlyLeuAspAlaasp 222
Oy 165 -----GAACCTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAACGTAAGTGG 112
    ||| ||| ||| ||| |||
Db 223 ArgLeuGluTrpAlaIleGluAlaAlaThrProAlaAspSerAlaAspSerThrValAl 242
Oy 111 TTGTGCTGCTCAATATACACATTAATAACACACAAACAATATGACGACCGTCC 52
    ||||| ||| ||||| |||
Db 243 -----ThrThrValGluGlyMecClYProthr 251

Oy 51 ATTATATCAGCATGGGACCGT 31
    :: ||||| |||
Db 252 LeuAlaValHisGlySerArg 258

RESULT 43
A71281
Probable S-adenosylmethionine synthetase (metk) - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 18-Jun-1999
C:Accession: A71281
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Wit-
  rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD-
  they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
C:Accession: A71281
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-396 <COL>
A:Cross-references: GB:AE001250; GB:AE000520; NID:93323096; PIDN:AC65758.1; PID:9332310
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0794
C:Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.: 4.89 Length: 396
Score: 59.00 Matches: 13
Percent Similarity: 54.55% Conservative: 5
Best Local Similarity: 39.39% Mismatches: 7
Query Match: 16.91% Indels: 8
DB: 2 Gaps: 2

US-09-198-779b-1 (1-235) x A71281 (1-396)
Oy 160 AGGTCATCAAGACCGCGCATACGGCCACTTGGCCGTGACGAC----- 204
    ||||| ||||| ||||| ||||| ||||| |||||
Db 355 ArgTYrArgSerThrAlaValTyrGlyHisPheGlyArgGlnPheProTrpGluArg 374
Oy 205 GCCGACTTCACCTCGGAGGTG-----GTCAGAGCC 234
    ||| ||||| ||||| ||||| |||||
Db 375 ThrAspCysValCysAspLeuGlnArgAlaValArgPro 387

RESULT 44
A47151
methionine adenosyltransferase (EC 2.5.1.6) - mouse
N:Alternate names: S-adenosylmethionine synthetase
C:Species: Mus musculus (house mouse)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-May-2000
C:Accession: A47151
R:Sakata, S.F.; Shelly, L.L.; Ruppert, S.; Schutz, G.; Chou, J.Y.
J. Biol. Chem. 268, 13978-13986, 1993
A:Title: Cloning and expression of murine S-adenosylmethionine synthetase.
A:Reference number: A47151; MUID:93300783; PMID:8314764
A:Accession: A47151

```

```

A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-396 <SAK>
A:Experimental source: liver
A>Note: sequence inconsistent with the nucleotide translation
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.: 4.89 Length: 396
Score: 59.00 Matches: 13
Percent Similarity: 71.43% Conservative: 2
Best Local Similarity: 61.90% Mismatches: 4
Query Match: 16.91% Indels: 2
DB: 2 Gaps: 1

US-09-198-779b-1 (1-235) x A47151 (1-396)
Oy 169 AAGACCGCCGATACGGCCACTTGGCCGTGACGACGCGGACTTCACCTGCGAGGTGTC 228
    ||||| ||||| ||||| ||||| ||||| |||||
Db 374 LysThrAlaCysTYrGlyHisPheGlyArg-----SerGluPheProTrpGluValPro 391
Oy 229 AAG 231
    |||
Db 392 Lys 392

RESULT 45
S06114
methionine adenosyltransferase (EC 2.5.1.6) - rat
N:Alternate names: S-adenosylmethionine synthetase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 05-May-2000
C:Accession: S06114; S18256; S18257
R:Hotikawa, S.; Ishikawa, M.; Ozasa, H.; Tsukada, K.
Eur. J. Biochem. 184, 497-501, 1989
A:Title: Isolation of a cDNA encoding the rat liver S-adenosylmethionine synthetase.
A:Reference number: S06114; MUID:90032633; PMID:2806235
C:Accession: S06114
A:Molecule type: mRNA
A:Residues: 1-397 <HOR>
A:Cross-references: EMBL:X15734; NID:957183; PIDN:CA433754.1; PID:957184
R:Mato, J.M.
submitted to the EMBL Data Library, July 1991
A:Reference number: S18256
A:Accession: S18256
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-397 <MAT>
A:Cross-references: EMBL:X60822
R:Alvarez, L.; Asuncion, M.; Corrales, F.; Pajares, M.A.; Mato, J.M.
FEBS Lett. 290, 142-146, 1991
A:Title: Analysis of the 5' non-coding region of rat liver S-adenosylmethionine synth
A:Reference number: S18257; MUID:92008649; PMID:1915866
C:Accession: S18257
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-46 <ALV>
A:Cross-references: EMBL:X60822
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.: 4.89 Length: 397
Score: 59.00 Matches: 13
Percent Similarity: 71.43% Conservative: 2
Best Local Similarity: 61.90% Mismatches: 4
Query Match: 16.91% Indels: 2
DB: 2 Gaps: 1

US-09-198-779b-1 (1-235) x S06114 (1-397)
Oy 169 AAGACCGCCGATACGGCCACTTGGCCGTGACGACGCGGACTTCACCTGCGAGGTGTC 228

```

```
Db 375 LysThrAlaCysTyrGlyHisPheGlyArg-----SeriGluPheProTyrGluValPro 392
QY 229 AAG 231
Db 393 Lys 393
```

Search completed: April 23, 2003, 12:07:53
Job time : 24.5833 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

```
Run on:      April 23, 2003, 12:06:52 ; Search time 55.9444 Seconds
              (without alignments)
              3059.318 Million cell updates/sec
```

Title: US-09-198-779B-1_COPY_160_235

Sequence: 1 aggttcatacaagaccgcgc.....ctgcgagtggtcaagcccc 76

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : N_Geneseq_101002:*

1:	/SID52/gcgdata/genseq/genseqn-emb1/NA1980.DAT *
2:	/SID52/gcgdata/genseq/genseqn-emb1/NA1981.DAT *
3:	/SID52/gcgdata/genseq/genseqn-emb1/NA1982.DAT *
4:	/SID52/gcgdata/genseq/genseqn-emb1/NA1983.DAT *
5:	/SID52/gcgdata/genseq/genseqn-emb1/NA1984.DAT *
6:	/SID52/gcgdata/genseq/genseqn-emb1/NA1985.DAT *
7:	/SID52/gcgdata/genseq/genseqn-emb1/NA1986.DAT *
8:	/SID52/gcgdata/genseq/genseqn-emb1/NA1987.DAT *
9:	/SID52/gcgdata/genseq/genseqn-emb1/NA1988.DAT *
10:	/SID52/gcgdata/genseq/genseqn-emb1/NA1989.DAT *
11:	/SID52/gcgdata/genseq/genseqn-emb1/NA1990.DAT *
12:	/SID52/gcgdata/genseq/genseqn-emb1/NA1991.DAT *
13:	/SID52/gcgdata/genseq/genseqn-emb1/NA1992.DAT *
14:	/SID52/gcgdata/genseq/genseqn-emb1/NA1993.DAT *
15:	/SID52/gcgdata/genseq/genseqn-emb1/NA1994.DAT *
16:	/SID52/gcgdata/genseq/genseqn-emb1/NA1995.DAT *
17:	/SID52/gcgdata/genseq/genseqn-emb1/NA1996.DAT *
18:	/SID52/gcgdata/genseq/genseqn-emb1/NA1997.DAT *
19:	/SID52/gcgdata/genseq/genseqn-emb1/NA1998.DAT *
20:	/SID52/gcgdata/genseq/genseqn-emb1/NA1999.DAT *
21:	/SID52/gcgdata/genseq/genseqn-emb1/NA2000.DAT *
22:	/SID52/gcgdata/genseq/genseqn-emb1/NA2001A.DAT *
23:	/SID52/gcgdata/genseq/genseqn-emb1/NA2001B.DAT *
24:	/SID52/gcgdata/genseq/genseqn-emb1/NA2002.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	74.4	97.9	1674	21	AAAC47744	Zea mays DNA fragm
2	64.8	85.3	1380	20	AAK07185	Wheat S-adenosylme
3	61.6	81.1	1182	19	AAI991413	S-adenosylmethionin
4	60	78.9	1182	19	AAI991413	S-adenosylmethionin
5	58.4	76.8	1182	19	AAI991412	S-adenosylmethionin
6	53.6	70.5	399	20	AAK81128	S-adenosyl methion
7	52	68.4	1485	20	AAK07184	Soybean S-adenosyl
8	52	68.4	1518	21	AAA51037	Soybean S-adenosyl
9	51	67.1	1582	20	AAK07183	Corn S-adenosylme

10	50.4	66.3	635	21	AAC44219	Arabidopsis thaliana
11	50.4	66.3	1508	21	AAC33986	Arabidopsis thaliana
12	50.4	66.3	1521	21	AAC45478	Arabidopsis thaliana
13	50.4	66.3	1529	21	AAC33535	Arabidopsis thaliana
14	48.8	64.2	1653	21	AAC45944	Arabidopsis thaliana
15	48.8	64.2	1654	21	AAC35348	Arabidopsis thaliana
16	42.4	60.0	1636	22	AAD02296	Arabidopsis thaliana
17	42.4	55.8	1393	21	AAC36421	Nicotiana tabacum
18	42.4	55.8	1395	21	AAC33674	Arabidopsis thaliana
19	38.2	50.3	4848	24	AAD22684	Arabidopsis thaliana
20	38.2	50.3	4848	24	AAD22686	Streptomyces fradi
21	37.6	49.5	1693	21	AAAF5637	Streptomyces fradi
22	37.6	49.5	1693	21	AAZ56005	Nucleotide sequenc
23	37.4	49.2	297	24	AB172111	Contig_004 from co
24	37.4	49.2	1208	15	AAOC4204	corn tassels-derive
25	37.4	49.2	5392	15	AAOC4201	snac gene encoding
26	34.4	45.3	4403765	22	AAAG6482	mycobacterium complisn
27	34.4	45.3	4411529	22	AA199683	Mycobacterium tub
28	32.8	43.2	56485	21	AAAF1612	Mycobacterium tub
29	32.8	43.2	349980	21	AAAF2161	N. meningitidis pa
30	32.8	43.2	837096	21	AAAB1489	Neisseria meningit
31	30.6	40.3	606	23	AAAS1580	N. meningitidis pa
32	28.6	37.6	657	21	AAAF1246	Pseudomonas aerugi
33	27.8	36.6	383	21	AAAF08069	Aspergillus oryzae
34	27.8	36.6	2284	24	ABK13571	Fusarium venenatum
35	27.8	36.6	3600	17	AAK13227	Ryegrass 4-coumar
36	27.8	36.6	7584	20	AAAI9362	Thermotoga enzymb
37	27.8	36.6	7600	21	AAAS1878	Rhodococcus corall
38	27.6	36.3	1957	22	AAAD0794	Rhodococcus sp. OH
39	27.6	36.3	2907	24	ABO90584	Rice cysteinyl-tRN
40	27.4	36.1	1791	20	AAZ25737	N. capsulatus gene
41	27.4	36.1	1791	20	AAZ27601	Stachybotrys chart
42	27.4	36.1	1791	21	AAAF0019	Stachybotrys pheno
43	27.4	36.1	1791	21	AAAS1314	Stachybotrys chart
44	27.4	36.1	1791	21	AAAS1314	Stachybotrys chart
45	27.4	36.1	7248	24	ABAA2911	S. chartarum phenol
46	27.2	35.8	566	21	AAAF08527	Stachybotrys chart
47	27.2	35.8	1104	23	AB102251	Fusarium venenatum
48	27.2	35.8	3178	23	AB102250	Drosophila melanog
49	27	35.5	5675	19	AAAT7186	Drosophila melanog
50	27	35.5	53789	19	AAV21187	Amycopilopsis medi
					AAV21187	Amycopilopsis medi

ALIGNMENTS

```

RESULT 1
AAC47744
ID AAC47744 standard; DNA; 1674 BP

```

AAC47744;

18-OCT-2000 (first entry)

Zea mays DNA fragment SEQ ID NO: 54954.

Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic

Zea mays subsp. *mays*

EP1033405-A2

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

25-FEB-1999; 99US-0121825.
05-MAR-1999; 99US-0123780

09-MAR-1999; 99US-0123548.
23-MAR-1999; 99US-0125788

25-MAR-1999; 9905-0126264.

PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140655.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145921.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155559.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.

```

PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

```

Query Match          97.9%; Score 74.4; DB:21; Length 1674;
Best Local Similarity 98.7%; Pred. No. 5.5e-14;
Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 1 AGGTCATCAGACGCCGCGCATACGCGCACTTGGCCGTGAGAGAGCCGACCTTCACTGC 60
    |||||
DB 1188 AGGTCATCAGACGCCGCGCATACGCGCACTTGGCCGTGAGAGAGCCGACCTTCACTGC 1247
    |||||
OY 61 GAGGTGCTCAAGCCCC 76
    |||||
DB 1248 GAGGTGCTCAAGCCCC 1263

```

```

RESULT 2
AA07185
ID AA07185 standard; cDNA; 1380 BP.
XX
AC AA07185;
XX
DT 21-MAY-1999 (first entry)
XX
DE

```

Wheat S-adenosylmethionine synthetase cDNA contig.

KM S-adenosylmethionine synthetase; wheat; amino acid; lysine;
 KM threonine; methionine; cysteine; isoleucine; transgenic plant;
 KM crop improvement; food; feedstuff; ss.

OS Triticum aestivum.

XX
 FT Key Location/Qualifiers
 FT CDS 73..1257 /*tag= a

XX MO9855601-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11692.

XX 12-JUN-1997; 97US-0049443.

XX 06-JUN-1997; 97US-0048771.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

```

XX Abell LM, Allen SM, Falco SC, Hitz WD, Kinney AJ;
PI Rafalski JA, Thorpe CJ;
XX WPI: 1999-070263/06.
DR P-PSDB: AAW97744.
XX
XX New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
PT encode: dihydropicolinate reductase; diaminopimelate epimerase;
PT threonine synthase; threonine deaminase; S-adenosylmethionine
PT synthetase
XX
PS Claim 47; Page 69-70; 98pp; English.
XX
XX This is the nucleotide sequence of a cDNA contig that codes for
XX a full-length wheat S-adenosylmethionine synthetase (see AAW97744).
XX The contig was assembled from clones isolated from wheat kernel,
XX leaf, seedling and root cDNA libraries and identified by comparison
XX to public sequence databases using BLAST algorithms. It shows
XX sequence similarity to the barley enzyme. The invention relates to
XX new isolated nucleic acid fragments (see AA07168-85) encoding plant
XX enzymes (see AAW97727-44) that catalyze steps in the biosynthesis of
XX lysine, threonine, methionine, cysteine and isoleucine from
XX aspartate, the enzyme being selected from dihydropicolinate reductase,
XX diaminopimelate epimerase, threonine synthase, threonine deaminase
XX or S-adenosylmethionine synthetase. The invention also relates to
XX the construction of a chimeric gene encoding all or a portion of
XX the biosynthetic pathway enzyme, in sense or antisense orientation,
XX where expression of the chimeric gene results in production of
XX altered levels of the enzyme in a transformed host cell.
XX Overexpression or reduction of expression of genes encoding the
XX amino acid biosynthetic pathway enzymes in crop plants such as
XX corn, soybean and wheat can be used to alter levels of the amino
XX acids in human food and animal feed. Transformed host cells can
XX also be used to identify compounds that inhibit one of the enzymes.
XX
SQ Sequence 1380 BP; 299 A; 430 C; 379 G; 267 T; 5 other;

```

```

Query Match          85.3%; Score 64.8; DB:20; Length 1380;
Best Local Similarity 90.8%; Pred. No. 5.2e-11;
Matches 69; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

OY 1 AGGTCATCAGACGCCGCGCATACGCGCACTTGGCCGTGAGAGAGCCGACCTTCACTGC 60
    |||||
DB 1156 AGGTCATCAGACGCCGCGCATACGCGCACTTGGCCGTGAGAGAGCCGACCTTCACTGC 1215
    |||||
OY 61 GAGGTGCTCAAGCCCC 76
    |||||
DB 1216 GAGGTGCTCAAGCCCC 1231

```

```

RESULT 3
AAT99143
ID AAT99143 standard; cDNA to mRNA; 1182 BP.
XX
AC AAT99143;
XX
DT 26-MAR-1998 (first entry)
XX
DE

```

S-adenosylmethionine synthase 3 gene.

KM S-adenosylmethionine synthase 3 gene; barley; alkali resistant plant;
 KM sam3; ss.

OS Hordeum vulgare.

XX JP09313186-A.

XX 09-DEC-1997.

XX 28-MAY-1996; 96JP-0133406.

XX 28-MAY-1996; 96JP-0133406.

XX (NIOC) NIPPON OIL CO LTD.
XX
XX WPI: 1998-080077/08.
DR P-PSDB: AAW34542.
XX
PT S-adenosyl-methionine synthase gene - useful in producing plants
resistant to alkaline soil
XX
XX Claim 6; Page 10-11; 13pp; Japanese.
PS
CC This sequence represents the S-adenosylmethionine synthase 3 (sam3)
CC gene. This DNA sequence may be used in a vector to produce plants which
are resistant to alkaline soil.
CC
SQ Sequence 1182 BP; 253 A; 368 C; 331 G; 230 T; 0 other;

Query Match 81.1%; Score 61.6; DB 19; Length 1182;
Best Local Similarity 86.2%; Pred. No. 5.1e-10;
Matches 67; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 AGGTTTCATCAGACCCCGCATACGCGCCTTTGGCCGTGACGACGCCGACTTCACCTGC 60
DB 1084 AGGTTTCATCAGACGACGCTGTTATGCTCACTTTGGCCGAGCATGCCACTTCACCTGG 1143
QY 61 GAGGTGTCAGACCCC 76
DB 1144 GAGGTGTCAGACCCC 1159

RESULT 4
AAT99141
ID AAT99141 standard; cDNA to mRNA; 1182 BP.
XX
AC AAT99141;
XX
DT 26-MAR-1998 (first entry)
XX
DE S-adenosylmethionine synthase 1 gene.
XX
KW S-adenosylmethionine synthase 1 gene; barley; alkali resistant plant;
KW sam1; ss.
XX
OS Hordeum vulgare.
XX
PN JP09313186-A.
XX
PD 09-DEC-1997.
XX
PF 28-MAY-1996; 96JP-0133406.
XX
PR 28-MAY-1996; 96JP-0133406.
XX
PA (NIOC) NIPPON OIL CO LTD.
XX
DR WPI: 1998-080077/08.
DR P-PSDB: AAW34540.
XX
PT S-adenosyl-methionine synthase gene - useful in producing plants
resistant to alkaline soil
XX
PS Claim 4; Page 8-9; 13pp; Japanese.
XX
CC This sequence represents the S-adenosylmethionine synthase 1 (sam1)
CC gene. This DNA sequence may be used in a vector to produce plants which
are resistant to alkaline soil.
CC
SQ Sequence 1182 BP; 253 A; 372 C; 324 G; 233 T; 0 other;

Query Match 78.9%; Score 60; DB 19; Length 1182;
Best Local Similarity 86.8%; Pred. No. 1.6e-09;
Matches 66; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 AGGTTTCATCAGACCCCGCATACGCGCCTTTGGCCGTGACGACGCCGACTTCACCTGC 60
DB 1084 AGGTTTCATCAGACGACGCTGTTATGCTCACTTTGGCCGAGCATGCCACTTCACCTGG 1143
QY 61 GAGGTGTCAGACCCC 76
DB 1144 GAGGTGTCAGACCCC 1159

RESULT 5
AAT99142
ID AAT99142 standard; cDNA to mRNA; 1182 BP.
XX
AC AAT99142;
XX
DT 26-MAR-1998 (first entry)
XX
DE S-adenosylmethionine synthase 2 gene.
XX
KW S-adenosylmethionine synthase 2 gene; barley; alkali resistant plant;
KW sam2; ss.
XX
OS Hordeum vulgare.
XX
PN JP09313186-A.
XX
PD 09-DEC-1997.
XX
PF 28-MAY-1996; 96JP-0133406.
XX
PR 28-MAY-1996; 96JP-0133406.
XX
PA (NIOC) NIPPON OIL CO LTD.
XX
DR WPI: 1998-080077/08.
DR P-PSDB: AAW34541.
XX
PT S-adenosyl-methionine synthase gene - useful in producing plants
resistant to alkaline soil
XX
PS Claim 5; Page 9-10; 13pp; Japanese.
XX
CC This sequence represents the S-adenosylmethionine synthase 2 (sam2)
CC gene. This DNA sequence may be used in a vector to produce plants which
are resistant to alkaline soil.
CC
SQ Sequence 1182 BP; 261 A; 368 C; 324 G; 229 T; 0 other;

Query Match 76.8%; Score 58.4; DB 19; Length 1182;
Best Local Similarity 85.5%; Pred. No. 5e-09; Mismatches 11; Indels 0; Gaps 0;
Matches 65; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 AGGTTTCATCAGACCCCGCATACGCGCCTTTGGCCGTGACGACGCCGACTTCACCTGC 60
DB 1084 AGGTTTCATCAGACGACGCTGTTATGCTCACTTTGGCCGAGCATGCCACTTCACCTGG 1143
QY 61 GAGGTGTCAGACCCC 76
DB 1144 GAGGTGTCAGACCCC 1159

RESULT 6
AAx81128
ID AAx81128 standard; cDNA; 399 BP.
XX
AC AAx81128;
XX
DT 06-SEP-1999 (first entry)
XX
DE S-adenosyl methionine (SAM) partial cDNA sequence.
XX
KW Senescence-associated receptor-like protein kinase; sakr; sam gene; sag;
senescence-associated gene; plant senescence; promoter; pharmaceutical;

Query Match 78.9%; Score 60; DB 19; Length 1182;
Best Local Similarity 86.8%; Pred. No. 1.6e-09;
Matches 66; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

KW plant maturation; S-adenosyl methionine; flower; fruit development; ss.
 XX Phaseolus vulgaris.
 OS
 XX MO9929159-A1.
 PN
 XX 17-JUN-1999.
 PD
 XX 08-DEC-1998; 98WO-US25799.
 PF
 XX 08-DEC-1997; 97US-0067898.
 PR
 XX (VITA-) VITALITY BIOTECHNOLOGIES INC.
 PA
 XX Gepstein S, Hajuoje T, Rosner A;
 PI
 XX WPI: 1999-404873/34.
 DR
 XX P-PSDB; AAY21978.
 PT
 XX DNA encoding senescence-associated genes for a senescence
 PT receptor-like protein kinase
 PS
 XX Claim 18; Fig 4; 70pp; English.
 CC The invention relates to a senescence-associated receptor-like protein
 CC kinase (sark) gene. The sark gene is a senescence-associated gene (sag)
 CC and is expressed early in the plant senescence process. The sark gene
 CC promoter is useful for driving expression of foreign genes having a
 CC desired product, such as a pharmaceutical, during the process of plant
 CC maturation. The sark gene promoter can be used to drive expression of
 CC resistance genes against pathogens or pests during senescence when the
 CC plant is particularly susceptible to infection or infestation. The sark
 CC gene promoter may also be used to drive expression of a gene encoding an
 CC inhibitor of senescence. Plant senescence may be inhibited by use of
 CC antisense sark constructs. Over expression of the sag genes, using the
 CC sark or sam (S-adenosyl methionine) gene promoters is useful for
 CC induction of early senescence. This is useful to obtain flower or fruit
 CC development prior to specific pest onset, prior to undesirable cross-
 CC fertilization from related crops, at a specific time during storage or
 CC retail, or to avoid development of plant structures that are not of
 CC agronomic importance. The present sequence represents a partial cDNA
 CC clone of S-adenosyl methionine (SAM).
 CC
 XX Sequence 399 BP; 108 A; 80 C; 82 G; 129 T; 0 other;
 SQ
 Query Match 70.5%; Score 53.6; DB 20; Length 399;
 Best Local Similarity 81.6%; Pred. No. 1.4e-07;
 Matches 62; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 QY 1 AGTTTCATCAAGACCGCCGATACGGCCTTGGCCGTGACGAGCCGACTTCACCTGC 60
 DB 102 AGTTCTTGAAGACTGCTGCATATGACACTTCGCGACAGAGAGCGACTTCACATGG 161
 QY 61 GAGGTGCTCAAGCCCC 76
 DB 162 GAAGTGTCAAGCCCC 177
 Db
 RESULT 7
 ID AAX07184 standard; cDNA; 1485 BP.
 AC AAX07184;
 XX
 XX 21-MAY-1999 (first entry)
 DE Soybean S-adenosylmethionine synthetase cDNA clone s2.12b06.
 XX
 XX S-adenosylmethionine synthetase; soybean; amino acid; lysine;
 KW threonine; methionine; cysteine; isoleucine; transgenic plant;
 KW crop improvement; food; feedstuff; ss.
 XX
 XX Glycine max.
 OS

XX Key Location/Qualifiers
 FH CDS 74..1252
 FT CDS /*tag= a
 ET
 XX MO9855601-A2.
 PN
 XX 10-DEC-1998.
 PD
 XX 05-JUN-1998; 98WO-US11692.
 PF
 XX 12-JUN-1997; 97US-0049443.
 PR
 XX 06-JUN-1997; 97US-0048771.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX
 XX Abell LM, Allen SM, Falco SC, Hiltz WD, Kinney AJ;
 PI Rafalski JA, Thorpe CJ;
 XX
 XX WPI: 1999-070263/06.
 DR
 XX P-PSDB; AAW97743.
 PT
 XX New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
 PT encode: dihydropicolinate reductase; diaminopimelate epimerase;
 PT threonine synthase; threonine deaminase; S-adenosylmethionine
 PT synthetase
 PS
 XX Claim 44; Page 66-67; 98pp; English.
 CC This is the nucleotide sequence of cDNA clone s2.12b06, which
 CC codes for a full-length soybean S-adenosylmethionine synthetase
 CC (see AAW97743). The clone was isolated from a soybean seed cDNA
 CC library and identified by comparison to public sequence databases
 CC using BLAST algorithms. It shows sequence similarity to the
 CC tomato enzyme. The invention relates to new isolated nucleic
 CC acid fragments (see AAX07168-85) encoding plant enzymes (see
 CC AAW97727-44) that catalyze steps in the biosynthesis of lysine,
 CC threonine, methionine, cysteine and isoleucine from aspartate, the
 CC enzyme being selected from dihydropicolinate reductase,
 CC diaminopimelate epimerase, threonine synthase, threonine deaminase
 CC or S-adenosylmethionine synthetase. The invention also relates to
 CC the construction of a chimeric gene encoding all or a portion of
 CC the biosynthetic pathway enzyme, in sense or antisense orientation,
 CC where expression of the chimeric gene results in production of
 CC altered levels of the enzyme in a transformed host cell.
 CC Overexpression or reduction of expression of genes encoding the
 CC amino acid biosynthetic pathway enzymes in crop plants such as
 CC corn, soybean and wheat can be used to alter levels of the amino
 CC acids in human food and animal feed. Transformed host cells can
 CC also be used to identify compounds that inhibit one of the enzymes.
 CC
 XX Sequence 1485 BP; 366 A; 373 C; 357 G; 389 T; 0 other;
 SQ
 Query Match 68.4%; Score 52; DB 20; Length 1485;
 Best Local Similarity 80.3%; Pred. No. 5.1e-07;
 Matches 61; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 1 AGTTTCATCAAGACCGCCGATACGGCCTTGGCCGTGACGAGCCGACTTCACCTGC 60
 DB 1157 AGTTCTTGAAGACTGCTGCATATGACACTTCGCGACAGAGAGCGACTTCACATGG 1216
 QY 61 GAGGTGCTCAAGCCCC 76
 DB 1217 GAAGTGTCAAGCCCC 1232
 Db
 RESULT 8
 ID AAA51037 standard; cDNA; 1518 BP.
 AC AAA51037;
 XX
 XX 09-OCT-2000 (first entry)
 DT

XX Soybean S-adenosyl-L-methionine synthetase cDNA.
 DE
 XX
 KW S-adenosyl-L-methionine synthetase; SAMS; probe; promoter; embryo;
 KM constitutive; tissue-specific; development-specific;
 KW herbicide resistance; pathogen resistance; ss.
 XX
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..73 /tag= a
 FT CDS 74..1252 /tag= b
 FT /product= S-adenosyl-L-methionine_synthetase
 XX
 PN WO200037662-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 17-DEC-1999; 99WO-US30180.
 XX
 PR 21-DEC-1998; 98US-0113045.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Falco SC, Li Z;
 DR WPI: 2000-442682/38.
 XX
 PT S-adenosyl-L-methionine synthetase promoter for expressing target
 PT heterologous herbicide-resistance or pathogen-resistance nucleic acid
 PT fragments in plants, especially soybean
 XX
 PS Example 2; Page 39; 50pp: English.
 XX
 CC This is the soybean full-length S-adenosyl-L-methionine synthetase (SAMS)
 CC cDNA, which was used to generate a probe to isolate a SAMS promoter. The
 CC SAMS promoter is active in seedlings and callus and over-expression of a
 CC gene in embryo stage can be achieved at an early developing stage using
 CC the SAMS promoter. The SAMS promoter may be used as an alternative to
 CC cauliflower mosaic virus 35S promoter to drive expression of selectable
 CC marker genes. Plant cells transformed with the SAMS constitutive promoter
 CC are useful for increasing or decreasing the expression of heterologous
 CC nucleic acid fragments in a plant, preferably corn, rice, wheat, barley,
 CC palm, Arabidopsis, soybean, oil seed Brassica, peanut, sunflower,
 CC safflower, cotton, tobacco, tomato, potato or cocoa. Target heterologous
 CC nucleic acid fragments include herbicide or pathogen resistance
 CC nucleic acid fragments.
 XX
 SQ Sequence 1518 BP; 399 A; 373 C; 357 G; 389 T; 0 other;
 Query Match 68.4%; Score 52; DB 21; Length 1518;
 Best Local Similarity 80.3%; Pred. No. 5.1e-07;
 Matches 61; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 1 AGGTCATCAAGACCGCCGACATGCGCCGTCGACGAGCCGACTTCACCTGC 60
 DB 1157 AGGTCATCAAGACCGCCGACATGCGCCGTCGACGAGCCGACTTCACCTGC 60
 QY 61 GAGTGCTCAAGCCCC 76
 DB 1217 GAGTGCTCAAGCCCC 1232
 RESULT 9
 AAX07183
 ID AAX07183 standard; cDNA; 1582 BP.
 XX
 AC AAX07183;
 XX
 DT 21-MAY-1999 (first entry)
 XX

DE Corn S-adenosylmethionine synthetase cDNA clone cc3.mn0002.d2.
 XX
 KW S-adenosylmethionine synthetase; corn; maize; amino acid; lysine;
 KM threonine; methionine; cysteine; isoleucine; transgenic plant;
 KW crop improvement; food; feedstuff; ss.
 XX
 OS Zea mays.
 XX
 FH Key Location/Qualifiers
 FT CDS 140..1330 /tag= a
 FT
 XX
 PN W09855601-A2.
 XX
 PD 10-DEC-1998.
 XX
 PF 05-JUN-1998; 98WO-US11692.
 XX
 PR 12-JUN-1997; 97US-0049443.
 PR 06-JUN-1997; 97US-0048771.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Abell LM, Allen SM, Falco SC, Hitz WD, Kinney AJ;
 PI Rafalski JA, Thorpe CJ;
 DR WPI: 1999-070263/06.
 DR P-PSDB; AAW97742.
 XX
 PT New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
 PT encode: dihydripycolinate reductase; diaminoepimerase;
 PT threonine synthase; threonine deaminase; S-adenosylmethionine
 PT synthetase
 XX
 PS Claim 41; Page 62-63; 98pp: English.
 XX
 CC This is the nucleotide sequence of cDNA clone cc3.mn0002.d2, which
 CC codes for a full-length corn S-adenosylmethionine synthetase
 CC (see AAW97742). The clone was isolated from a corn callus cDNA
 CC library and identified by comparison to public sequence databases
 CC using BLAST algorithms. It shows sequence similarity to the
 CC Oryza sativa enzyme. The invention relates to new isolated
 CC nucleic acid fragments (see AAX07168-85) encoding plant enzymes (see
 CC AAW97727-44) that catalyze steps in the biosynthesis of lysine,
 CC threonine, methionine, cysteine and isoleucine from aspartate, the
 CC enzyme being selected from dihydripycolinate reductase,
 CC diaminoepimerase, threonine synthase, threonine deaminase
 CC or S-adenosylmethionine synthetase. The invention also relates to
 CC the construction of a chimeric gene encoding all or a portion of
 CC the biosynthetic pathway enzyme, in sense or antisense orientation,
 CC where expression of the chimeric gene results in production of
 CC altered levels of the enzyme in a transformed host cell.
 CC Overexpression or reduction of expression of genes encoding the
 CC amino acid biosynthetic pathway enzymes in crop plants such as
 CC corn, soybean and wheat can be used to alter levels of the amino
 CC acids in human food and animal feed. Transformed host cells can
 CC also be used to identify compounds that inhibit one of the enzymes.
 XX
 SQ Sequence 1582 BP; 340 A; 474 C; 417 G; 351 T; 0 other;
 Query Match 67.1%; Score 51; DB 20; Length 1582;
 Best Local Similarity 80.0%; Pred. No. 1e-06;
 Matches 60; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 2 GGTTCATCAAGACCGCCGACATGCGCCGTCGACGAGCCGACTTCACCTGCG 61
 DB 1230 GGTTCATCAAGACCGCCGACATGCGCCGTCGAGGAGGACGACCTGACTGCGG 1289
 QY 62 AGTGCTCAAGCCCC 76
 DB 1290 AGTGCTCAAGCCCC 1304

RESULT 10
AAC44219
ID AAC44219 standard; DNA: 635 BP.
XX AAC44219;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 42062.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142927.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145149.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145911.
PR 28-JUL-1999; 99US-0145913.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.

```
PR 20-AUG-1999: 99US-0149929.
PR 23-AUG-1999: 99US-0149902.
PR 23-AUG-1999: 99US-0149930.
PR 25-AUG-1999: 99US-0150566.
PR 26-AUG-1999: 99US-0150884.
PR 27-AUG-1999: 99US-0151065.
PR 27-AUG-1999: 99US-0151066.
PR 27-AUG-1999: 99US-0151080.
PR 30-AUG-1999: 99US-0151303.
PR 31-AUG-1999: 99US-0151438.
PR 01-SEP-1999: 99US-0151930.
PR 07-SEP-1999: 99US-0152363.
PR 10-SEP-1999: 99US-0153070.
PR 13-SEP-1999: 99US-0153758.
PR 15-SEP-1999: 99US-0154018.
PR 16-SEP-1999: 99US-0154039.
PR 20-SEP-1999: 99US-0154779.
PR 22-SEP-1999: 99US-0155139.
PR 23-SEP-1999: 99US-0155486.
PR 24-SEP-1999: 99US-0155659.
PR 28-SEP-1999: 99US-0156458.
PR 29-SEP-1999: 99US-0156596.
PR 04-OCT-1999: 99US-0157117.
PR 05-OCT-1999: 99US-0157753.
PR 06-OCT-1999: 99US-0157865.
PR 07-OCT-1999: 99US-0158029.
PR 08-OCT-1999: 99US-0158232.
PR 12-OCT-1999: 99US-0158369.
PR 13-OCT-1999: 99US-0159293.
PR 13-OCT-1999: 99US-0159294.
PR 13-OCT-1999: 99US-0159295.
PR 14-OCT-1999: 99US-0159329.
PR 14-OCT-1999: 99US-0159330.
PR 14-OCT-1999: 99US-0159331.
PR 14-OCT-1999: 99US-0159637.
PR 18-OCT-1999: 99US-0159638.
PR 18-OCT-1999: 99US-0159584.
PR 21-OCT-1999: 99US-0160741.
PR 21-OCT-1999: 99US-0160767.
PR 21-OCT-1999: 99US-0160768.
PR 21-OCT-1999: 99US-0160770.
PR 21-OCT-1999: 99US-0160814.
PR 21-OCT-1999: 99US-0160815.
PR 22-OCT-1999: 99US-0160980.
PR 22-OCT-1999: 99US-0160981.
PR 22-OCT-1999: 99US-0160989.
PR 25-OCT-1999: 99US-0161404.
PR 25-OCT-1999: 99US-0161405.
PR 25-OCT-1999: 99US-0161406.
PR 26-OCT-1999: 99US-0161359.
PR 26-OCT-1999: 99US-0161360.
PR 26-OCT-1999: 99US-0161361.
PR 28-OCT-1999: 99US-0161920.
PR 28-OCT-1999: 99US-0161992.
PR 28-OCT-1999: 99US-0161993.
PR 29-OCT-1999: 99US-0162142.
```

Query Match 66.3%; Score 50.4; DB 21; Length 635;

Best Local Similarity 78.9%; Pred. No. 1.5e-06;

Matches 60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
QY 1 AGGTTATCAAGACCGCGATACGCGCACTTGGCCGTCAGACGCGCATTCACCTTC 60
Db 282 AGCTTTTAAAGACTGCTGCTATGCTCACTTTGAGAGGAGCATGCTGATTTCACTTGG 341
QY 61 GAGGTGTCACAGCCCC 76
Db 342 GAGGTAGTCACAGCCAC 357
```

RESULT 11
AAC33986
ID AAC33986 standard; DNA; 1508 BP.

```
XX AAC33986;
AC 17-OCT-2000 (first entry)
DT XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 5035.
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX 06-SEP-2000.
PD XX
PF 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132485.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139452.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
```

PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144881.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.

PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 29-OCT-1999; 99US-0162142.

Query Match 66.3%; Score 50.4; DB 21; Length 1508;
Best Local Similarity 78.9%; Pred. No. 1.6e-06;
Matches 60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AGGTTTCATCAAGACGCGCCATAGCGGCACCTTGGCCCGAGCAGCCGCACTTCACTTC 60
Db 1170 AGGTTTCATCAAGACGCGCCATAGCGGCACCTTGGAGGAGCAGATGCTGATTTCACTTCG 1229
QY 61 GAGGTGTCACGCCCC 76
Db 1230 GAGGTGTCACGCCCC 1245

RESULT 12
AAC45478
ID AAC45478 standard; DNA; 1521 BP.
XX
AC AAC45478;
XX

DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 46638.
DE
XX Hybridisation assay: genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX EPI033405-A2.
PN 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136382.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138340.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139482.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.

```
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157573.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
```

Query Match 66.3%; Score 50.4; DB 21; Length 1521;
Best Local Similarity 78.9%; Pred No. 1.6e-06;
Matches 60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
QY 1 AGGTTATCAAGAGCGCGCATATGCGCCTTGCGAGGAGCGACCTTCACTTCACCTGC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1168 AGGTTCTTGAACAGCTGCTCATGTGCTCATTGGAGAGGAGAGATGCTATTTCACCTGG 1227
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GAGGTGTCACGCCCC 76
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1228 GAGGTAGTCACGCCAC 1243
```

RESULT 13
AAC33535
ID AAC33535 standard; DNA; 1529 BP.
XX
AC AAC33535;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 3408.

```
XX Hybridisation assay; generic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN Ep1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0128845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134216.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.
```

```

PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143642.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149729.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.

```

```

PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161952.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

```

Query Match 66.3% Score 50.4; DB 21; Length 1529;
Best Local Similarity 78.9% Pred. No. 1.6e-06;
Matches 60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```

```

QY 1 AGGTCATCAAGACCGCGCATAGCGCCACTTGGCCGTGACGACGCCGACTTCACCTGC 60
DB 1210 AGGCTCTTGAACACGCGCGCTTACGACACTTTGGAGAGACGACCTGACTTCACCTGG 1269

```

```

QY 61 GAGGTGTCAGACCCC 76
DB 1270 GAACTGTCAGACCCAC 1285

```

```

RESULT 14
AAC45944
ID AAC45944 standard; DNA; 1653 BP.

```

```

AC AAC45944;

```

```

XX 18-OCT-2000 (first entry)

```

```

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 48340.

```

```

DE Hybridisation assay: genetic mapping; gene expression control;

```

```

KW protein identification; signal transduction pathway;

```


metabolic pathway; promoter; termination sequence; ss.
Arabidopsis thaliana.
EP1033405-A2.
06-SEP-2000.
25-FEB-2000; 2000EP-0301439.
25-FEB-1999; 99US-0121825.
05-MAR-1999; 99US-0123160.
09-MAR-1999; 99US-0123548.
23-MAR-1999; 99US-0125788.
25-MAR-1999; 99US-0126264.
29-MAR-1999; 99US-0126785.
01-APR-1999; 99US-0127462.
06-APR-1999; 99US-0128234.
08-APR-1999; 99US-0128714.
16-APR-1999; 99US-0129845.
19-APR-1999; 99US-0130077.
21-APR-1999; 99US-0130449.
23-APR-1999; 99US-0130510.
28-APR-1999; 99US-0130891.
30-APR-1999; 99US-0131449.
30-APR-1999; 99US-0132048.
04-MAY-1999; 99US-0132407.
05-MAY-1999; 99US-0132484.
06-MAY-1999; 99US-0132485.
06-MAY-1999; 99US-0132486.
06-MAY-1999; 99US-0132487.
07-MAY-1999; 99US-0132863.
11-MAY-1999; 99US-0134256.
14-MAY-1999; 99US-0134218.
14-MAY-1999; 99US-0134219.
14-MAY-1999; 99US-0134221.
14-MAY-1999; 99US-0134370.
18-MAY-1999; 99US-0134768.
19-MAY-1999; 99US-0134941.
20-MAY-1999; 99US-0135124.
21-MAY-1999; 99US-0135353.
24-MAY-1999; 99US-0135629.
25-MAY-1999; 99US-0136021.
27-MAY-1999; 99US-0136392.
28-MAY-1999; 99US-0136782.
01-JUN-1999; 99US-0137222.
03-JUN-1999; 99US-0137528.
04-JUN-1999; 99US-0137502.
07-JUN-1999; 99US-0137724.
08-JUN-1999; 99US-0138094.
10-JUN-1999; 99US-0138540.
10-JUN-1999; 99US-0138847.
14-JUN-1999; 99US-0139119.
16-JUN-1999; 99US-0139452.
16-JUN-1999; 99US-0139453.
17-JUN-1999; 99US-0139492.
18-JUN-1999; 99US-0139454.
18-JUN-1999; 99US-0139455.
18-JUN-1999; 99US-0139456.
18-JUN-1999; 99US-0139457.
18-JUN-1999; 99US-0139458.
18-JUN-1999; 99US-0139459.
18-JUN-1999; 99US-0139460.
18-JUN-1999; 99US-0139461.
18-JUN-1999; 99US-0139462.
18-JUN-1999; 99US-0139463.
18-JUN-1999; 99US-0139750.
18-JUN-1999; 99US-0139763.
21-JUN-1999; 99US-0139817.
22-JUN-1999; 99US-0139899.
23-JUN-1999; 99US-0140353.
23-JUN-1999; 99US-0140354.
24-JUN-1999; 99US-0140695.
28-JUN-1999; 99US-0140823.
29-JUN-1999; 99US-0140991.
30-JUN-1999; 99US-0141287.
01-JUL-1999; 99US-0141842.
01-JUL-1999; 99US-0142154.
02-JUL-1999; 99US-0142055.
06-JUL-1999; 99US-0142390.
08-JUL-1999; 99US-0142803.
09-JUL-1999; 99US-0142920.
12-JUL-1999; 99US-0142977.
13-JUL-1999; 99US-0143542.
14-JUL-1999; 99US-0143624.
15-JUL-1999; 99US-0144005.
16-JUL-1999; 99US-0144085.
16-JUL-1999; 99US-0144086.
19-JUL-1999; 99US-0144325.
19-JUL-1999; 99US-0144331.
19-JUL-1999; 99US-0144332.
19-JUL-1999; 99US-0144333.
19-JUL-1999; 99US-0144334.
19-JUL-1999; 99US-0144335.
20-JUL-1999; 99US-0144352.
20-JUL-1999; 99US-0144632.
20-JUL-1999; 99US-0144884.
21-JUL-1999; 99US-0144814.
21-JUL-1999; 99US-0145086.
21-JUL-1999; 99US-0145088.
22-JUL-1999; 99US-0145085.
22-JUL-1999; 99US-0145087.
22-JUL-1999; 99US-0145089.
22-JUL-1999; 99US-0145192.
23-JUL-1999; 99US-0145145.
23-JUL-1999; 99US-0145218.
23-JUL-1999; 99US-0145224.
26-JUL-1999; 99US-0145276.
27-JUL-1999; 99US-0145913.
27-JUL-1999; 99US-0145918.
27-JUL-1999; 99US-0145919.
28-JUL-1999; 99US-0145951.
02-AUG-1999; 99US-0146386.
02-AUG-1999; 99US-0146388.
02-AUG-1999; 99US-0146389.
03-AUG-1999; 99US-0147038.
04-AUG-1999; 99US-0147204.
05-AUG-1999; 99US-0147302.
05-AUG-1999; 99US-0147192.
05-AUG-1999; 99US-0147260.
06-AUG-1999; 99US-0147302.
06-AUG-1999; 99US-0147416.
09-AUG-1999; 99US-0147493.
09-AUG-1999; 99US-0147935.
10-AUG-1999; 99US-0148171.
11-AUG-1999; 99US-0148319.
12-AUG-1999; 99US-0148341.
13-AUG-1999; 99US-0148565.
13-AUG-1999; 99US-0148684.
16-AUG-1999; 99US-0149368.
17-AUG-1999; 99US-0149175.
18-AUG-1999; 99US-0149426.
20-AUG-1999; 99US-0149722.
20-AUG-1999; 99US-0149723.
20-AUG-1999; 99US-0149929.
23-AUG-1999; 99US-0149902.
23-AUG-1999; 99US-0149930.
25-AUG-1999; 99US-0150566.
26-AUG-1999; 99US-0150884.
27-AUG-1999; 99US-0151066.
27-AUG-1999; 99US-0151065.
27-AUG-1999; 99US-0151080.
30-AUG-1999; 99US-0151303.
31-AUG-1999; 99US-0151438.
01-SEP-1999; 99US-0151930.
07-SEP-1999; 99US-0152363.

```
PR 10-SEP-1999; 9905-0153070.
PR 13-SEP-1999; 9905-0153758.
PR 15-SEP-1999; 9905-0154018.
PR 16-SEP-1999; 9905-0154039.
PR 20-SEP-1999; 9905-0154779.
PR 22-SEP-1999; 9905-0155139.
PR 23-SEP-1999; 9905-0155486.
PR 24-SEP-1999; 9905-0155659.
PR 28-SEP-1999; 9905-0156458.
PR 29-SEP-1999; 9905-0156596.
PR 04-OCT-1999; 9905-0157117.
PR 05-OCT-1999; 9905-0157753.
PR 06-OCT-1999; 9905-0157863.
PR 07-OCT-1999; 9905-0158029.
PR 08-OCT-1999; 9905-0158232.
PR 12-OCT-1999; 9905-0158369.
PR 13-OCT-1999; 9905-0159293.
PR 13-OCT-1999; 9905-0159294.
PR 13-OCT-1999; 9905-0159295.
PR 14-OCT-1999; 9905-0159329.
PR 14-OCT-1999; 9905-0159330.
PR 14-OCT-1999; 9905-0159331.
PR 14-OCT-1999; 9905-0159637.
PR 14-OCT-1999; 9905-0159638.
PR 18-OCT-1999; 9905-0159584.
PR 21-OCT-1999; 9905-0160741.
PR 21-OCT-1999; 9905-0160767.
PR 21-OCT-1999; 9905-0160768.
PR 21-OCT-1999; 9905-0160770.
PR 21-OCT-1999; 9905-0160814.
PR 21-OCT-1999; 9905-0160815.
PR 22-OCT-1999; 9905-0160980.
PR 22-OCT-1999; 9905-0160981.
PR 22-OCT-1999; 9905-0160989.
PR 25-OCT-1999; 9905-0161404.
PR 25-OCT-1999; 9905-0161405.
PR 25-OCT-1999; 9905-0161406.
PR 26-OCT-1999; 9905-0161359.
PR 26-OCT-1999; 9905-0161360.
PR 26-OCT-1999; 9905-0161361.
PR 28-OCT-1999; 9905-0161920.
PR 28-OCT-1999; 9905-0161992.
PR 28-OCT-1999; 9905-0161993.
PR 29-OCT-1999; 9905-0162142.
```

```
Query Match 64.2%; Score 48.8; DB 21; Length 1653;
Best Local Similarity 77.6%; Pred. No. 5,1e-06;
Matches 59; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
```

```
OY 1 AGCTTCATCAACACCGCCGACCTTGGCCGTGAGACGCCGACCTTCACCTGC 60
DB 1228 AGGTTCCAGAAACCGCTGATGCGCATTCGGCGGTGATGACCTTCACCTTGG 1287
OY 61 GAGGTGTCACGCC 76
DB 1288 GAGGTTGTCAACGCC 1303
```

```
RESULT 15
AAC35348
ID AAC35348 standard; DNA; 1654 BP.
XX AAC35348;
XX 17-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 9862.
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS
```

```
XX EPI033405-A2.
XX 06-SEP-2000.
PD 25-FEB-2000; 2000EP-0301439.
PF XX
XX 25-FEB-1999; 9905-0121825.
PR 05-MAR-1999; 9905-0123180.
PR 09-MAR-1999; 9905-0123548.
PR 23-MAR-1999; 9905-0125788.
PR 25-MAR-1999; 9905-0126264.
PR 29-MAR-1999; 9905-0126785.
PR 01-APR-1999; 9905-0127462.
PR 06-APR-1999; 9905-0128234.
PR 08-APR-1999; 9905-0128714.
PR 16-APR-1999; 9905-0129845.
PR 19-APR-1999; 9905-0130077.
PR 21-APR-1999; 9905-0130449.
PR 23-APR-1999; 9905-0130510.
PR 28-APR-1999; 9905-0130891.
PR 30-APR-1999; 9905-0131449.
PR 30-APR-1999; 9905-0132048.
PR 04-MAY-1999; 9905-0132407.
PR 05-MAY-1999; 9905-0132484.
PR 06-MAY-1999; 9905-0132485.
PR 06-MAY-1999; 9905-0132486.
PR 07-MAY-1999; 9905-0132487.
PR 11-MAY-1999; 9905-0134256.
PR 14-MAY-1999; 9905-0134218.
PR 14-MAY-1999; 9905-0134219.
PR 14-MAY-1999; 9905-0134221.
PR 14-MAY-1999; 9905-0134370.
PR 18-MAY-1999; 9905-0134768.
PR 19-MAY-1999; 9905-0134941.
PR 20-MAY-1999; 9905-0135124.
PR 21-MAY-1999; 9905-0135353.
PR 24-MAY-1999; 9905-0135629.
PR 25-MAY-1999; 9905-0136021.
PR 27-MAY-1999; 9905-0136392.
PR 28-MAY-1999; 9905-0136782.
PR 01-JUN-1999; 9905-0137223.
PR 03-JUN-1999; 9905-0137528.
PR 04-JUN-1999; 9905-0137502.
PR 07-JUN-1999; 9905-0137724.
PR 08-JUN-1999; 9905-0138094.
PR 10-JUN-1999; 9905-0138540.
PR 10-JUN-1999; 9905-0138847.
PR 14-JUN-1999; 9905-0139119.
PR 16-JUN-1999; 9905-0139452.
PR 16-JUN-1999; 9905-0139453.
PR 17-JUN-1999; 9905-0139492.
PR 18-JUN-1999; 9905-0139454.
PR 18-JUN-1999; 9905-0139455.
PR 18-JUN-1999; 9905-0139456.
PR 18-JUN-1999; 9905-0139457.
PR 18-JUN-1999; 9905-0139458.
PR 18-JUN-1999; 9905-0139459.
PR 18-JUN-1999; 9905-0139460.
PR 18-JUN-1999; 9905-0139461.
PR 18-JUN-1999; 9905-0139462.
PR 18-JUN-1999; 9905-0139463.
PR 18-JUN-1999; 9905-0139750.
PR 18-JUN-1999; 9905-0139763.
PR 21-JUN-1999; 9905-0139817.
PR 22-JUN-1999; 9905-0139859.
PR 23-JUN-1999; 9905-0140353.
PR 23-JUN-1999; 9905-0140354.
PR 24-JUN-1999; 9905-0140695.
PR 28-JUN-1999; 9905-0140823.
PR 29-JUN-1999; 9905-0140991.
PR 30-JUN-1999; 9905-0141287.
```

```

PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145226.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147182.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149358.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.

```

```

PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155486.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161358.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 29-OCT-1999; 99US-0162142.

```

Query Match 64.2%; Score 48.8; DB 21; Length 1654;
 Best Local Similarity 77.6%; Pred. No. 5,1e-06;
 Matches 59; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

```

OY 1 AGGTTCAATCAAGACCGCGGCATACGCGCCACTTTGGCCGTGACGAGCGCGACTTCACCTGC 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1229 AGGTTCAAGAAACCGCGCGATGCGCATTTCCGGCGTGATGACCTTCACCTTCG 1288
OY 61 GAGGTGTCAGAGCCCG 76
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1289 GAGGTGTCAGAGCCCG 1304

```

```

RESULT 16
AAD02296
ID AAD02296 standard; DNA; 1636 BP.
XX
AC AAD02296;
XX
DT 28-MAR-2001 (first entry)
DE Nicotiana tabacum S-adenosylmethionine synthetase (SAMS) DNA.
XX
KW Tobacco; alkaloid; nicotine; transgenic plant; pharmaceutical protein;
XX herbicide resistance; S-adenosylmethionine synthetase; SAMS; ds.
OS Nicotiana tabacum.
XX
FH Key Location/Qualifiers
FT CDS 96..1268
    /*tag= a

```

FT /product- "Nicotiana tabacum S-adenosylmethionine
synthetase (SAMS) protein"
XX WO200067558-A1.
XX
XX 16-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US12450.
XX
XX 06-MAY-1999; 99US-0132919.
XX
XX (TIMK/) TIMKO M.
XX
XX Timko M;
XX
XX WPI: 2001-0072279/01.
XX P-PSDB: AAY72078.
XX
XX New nucleic acid encoding alkaloid-synthesis enzymes in tobacco, useful
e.g. for producing transgenic plants with altered nicotine content
XX
XX Claim 1; Page 78-79; 103pp; English.
XX
XX The invention relates to enzymes involved in alkaloid, specifically
nicotine, synthesis in tobacco and nucleic acids encoding them. The
nucleic acid of the invention can be used, in sense or antisense
orientation, to produce transgenic tobacco plants with altered
alkaloid content, and also for expression of exogenous proteins,
e.g. pharmaceutical proteins or proteins implicated in resistance
to herbicides. The protein of the invention can be used to
identify modulators of enzymatic activity in plants.
XX The present sequence is Nicotiana tabacum S-adenosylmethionine
synthetase (SAMS) DNA. This enzyme is involved in the nicotine
biosynthetic pathway.
XX
XX Sequence 1636 BP; 444 A; 365 C; 373 G; 454 T; 0 other;
SO
Query Match 60.0%; Score 45.6; DB 22; Length 1636;
Best Local Similarity 75.0%; Pred. No. 5e-05;
Matches 57; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
OY 1 AGGTTATCAAGACGGCCGATACGCTTGGCCGAGACGGCGACTTCACCTGC 60
DB 1176 AGGTACAGAGACGCTAGCTTATGCTCAGCTTGCGCGATGCCGACTTCATCG 1235
OY 61 GAGGTGCTCAAGCCCC 76
DB 1236 GAGACTGTCAAGGTCC 1251
RESULT 17
AAC46421
ID AAC46421 standard; DNA; 1393 BP.
XX
XX AAC46421;
XX
XX 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 50076.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR

PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140635.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.

```

PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150864.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.

```

```

PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

```

Query Match 55.8%; Score 42.4; DB 21; Length 1393;
Best Local Similarity 72.4%; Pred. No. 0.00049;
Matches 55; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```

```

Qy 1 AGGTTTCATCAGACCGCGCATACGCCACCTTGGCCGTGACGAGCCGACTTCACCTGC 60
Db 1175 AGGTTTCAGAAACGGCGACCGCTATGACATTTTCGAGAGAGACGCCCTGACTTCACCTCG 1234

```

```

Qy 61 GAGGTGCTCAAGCCCC 76
Db 1235 GAGGTGCTGAGACCCAC 1250

```

```

RESULT 18
AAC3674
ID AAC3674 standard; DNA; 1395 BP.
XX
AC AAC3674;
XX

```

```

DT 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 3906.
DE
XX
XX

```

```

KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
XX

```

```

PD 06-SEP-2000;
XX
XX
XX

```

```

PF 25-FEB-2000; 2000EP-0301439.
XX
XX

```

```

PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123160.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.

```

PR 25-MAR-1999; 9905-0126264.
PR 29-MAR-1999; 9905-0126785.
PR 01-APR-1999; 9905-0127462.
PR 06-APR-1999; 9905-0128234.
PR 08-APR-1999; 9905-0128714.
PR 16-APR-1999; 9905-0129845.
PR 19-APR-1999; 9905-0130077.
PR 21-APR-1999; 9905-0130449.
PR 23-APR-1999; 9905-0130510.
PR 23-APR-1999; 9905-0130891.
PR 28-APR-1999; 9905-0131449.
PR 30-APR-1999; 9905-0132048.
PR 30-APR-1999; 9905-0132407.
PR 04-MAY-1999; 9905-0132484.
PR 05-MAY-1999; 9905-0132485.
PR 06-MAY-1999; 9905-0132486.
PR 06-MAY-1999; 9905-0132487.
PR 07-MAY-1999; 9905-0132863.
PR 11-MAY-1999; 9905-0134256.
PR 14-MAY-1999; 9905-0134218.
PR 14-MAY-1999; 9905-0134219.
PR 14-MAY-1999; 9905-0134221.
PR 14-MAY-1999; 9905-0134370.
PR 18-MAY-1999; 9905-0134768.
PR 19-MAY-1999; 9905-0134941.
PR 20-MAY-1999; 9905-0135124.
PR 21-MAY-1999; 9905-0135353.
PR 24-MAY-1999; 9905-0135629.
PR 25-MAY-1999; 9905-0136021.
PR 27-MAY-1999; 9905-0136392.
PR 28-MAY-1999; 9905-0136782.
PR 01-JUN-1999; 9905-0137222.
PR 03-JUN-1999; 9905-0137528.
PR 04-JUN-1999; 9905-0137502.
PR 07-JUN-1999; 9905-0137724.
PR 08-JUN-1999; 9905-0138094.
PR 10-JUN-1999; 9905-0138540.
PR 10-JUN-1999; 9905-0138847.
PR 14-JUN-1999; 9905-0139119.
PR 16-JUN-1999; 9905-0139452.
PR 16-JUN-1999; 9905-0139453.
PR 17-JUN-1999; 9905-0139454.
PR 18-JUN-1999; 9905-0139455.
PR 18-JUN-1999; 9905-0139456.
PR 18-JUN-1999; 9905-0139457.
PR 18-JUN-1999; 9905-0139458.
PR 18-JUN-1999; 9905-0139459.
PR 18-JUN-1999; 9905-0139460.
PR 18-JUN-1999; 9905-0139461.
PR 18-JUN-1999; 9905-0139462.
PR 18-JUN-1999; 9905-0139463.
PR 18-JUN-1999; 9905-0139750.
PR 18-JUN-1999; 9905-0139763.
PR 21-JUN-1999; 9905-0139817.
PR 22-JUN-1999; 9905-0139899.
PR 23-JUN-1999; 9905-0140353.
PR 23-JUN-1999; 9905-0140354.
PR 24-JUN-1999; 9905-0140695.
PR 28-JUN-1999; 9905-0140823.
PR 29-JUN-1999; 9905-0140991.
PR 30-JUN-1999; 9905-0141287.
PR 01-JUL-1999; 9905-0141842.
PR 01-JUL-1999; 9905-0142154.
PR 02-JUL-1999; 9905-0142055.
PR 06-JUL-1999; 9905-0142390.
PR 08-JUL-1999; 9905-0142803.
PR 09-JUL-1999; 9905-0142920.
PR 12-JUL-1999; 9905-0142977.
PR 13-JUL-1999; 9905-0143542.
PR 14-JUL-1999; 9905-0143624.
PR 15-JUL-1999; 9905-0144005.
PR 16-JUL-1999; 9905-0144085.

PR 16-JUL-1999; 9905-0144086.
PR 19-JUL-1999; 9905-0144325.
PR 19-JUL-1999; 9905-0144331.
PR 19-JUL-1999; 9905-0144332.
PR 19-JUL-1999; 9905-0144333.
PR 19-JUL-1999; 9905-0144334.
PR 19-JUL-1999; 9905-0144335.
PR 20-JUL-1999; 9905-0144352.
PR 20-JUL-1999; 9905-0144632.
PR 20-JUL-1999; 9905-0144884.
PR 21-JUL-1999; 9905-0144814.
PR 21-JUL-1999; 9905-0145086.
PR 21-JUL-1999; 9905-0145088.
PR 22-JUL-1999; 9905-0145085.
PR 22-JUL-1999; 9905-0145087.
PR 22-JUL-1999; 9905-0145089.
PR 22-JUL-1999; 9905-0145192.
PR 23-JUL-1999; 9905-0145145.
PR 23-JUL-1999; 9905-0145218.
PR 23-JUL-1999; 9905-0145224.
PR 26-JUL-1999; 9905-0145276.
PR 27-JUL-1999; 9905-0145913.
PR 27-JUL-1999; 9905-0145918.
PR 27-JUL-1999; 9905-0145919.
PR 28-JUL-1999; 9905-0145951.
PR 28-JUL-1999; 9905-0145951.
PR 02-AUG-1999; 9905-0146386.
PR 02-AUG-1999; 9905-0146388.
PR 02-AUG-1999; 9905-0146389.
PR 03-AUG-1999; 9905-0147038.
PR 04-AUG-1999; 9905-0147204.
PR 04-AUG-1999; 9905-0147302.
PR 05-AUG-1999; 9905-0147192.
PR 05-AUG-1999; 9905-0147260.
PR 06-AUG-1999; 9905-0147303.
PR 06-AUG-1999; 9905-0147416.
PR 09-AUG-1999; 9905-0147483.
PR 09-AUG-1999; 9905-0147935.
PR 10-AUG-1999; 9905-0148171.
PR 11-AUG-1999; 9905-0148319.
PR 12-AUG-1999; 9905-0148341.
PR 13-AUG-1999; 9905-0148565.
PR 13-AUG-1999; 9905-0148684.
PR 16-AUG-1999; 9905-0149368.
PR 17-AUG-1999; 9905-0149175.
PR 18-AUG-1999; 9905-0149426.
PR 20-AUG-1999; 9905-0149722.
PR 20-AUG-1999; 9905-0149723.
PR 20-AUG-1999; 9905-0149929.
PR 23-AUG-1999; 9905-0149902.
PR 23-AUG-1999; 9905-0149920.
PR 25-AUG-1999; 9905-0150566.
PR 26-AUG-1999; 9905-0150884.
PR 27-AUG-1999; 9905-0151065.
PR 27-AUG-1999; 9905-0151066.
PR 27-AUG-1999; 9905-0151080.
PR 30-AUG-1999; 9905-0151303.
PR 31-AUG-1999; 9905-0151438.
PR 01-SEP-1999; 9905-0151930.
PR 07-SEP-1999; 9905-0152363.
PR 10-SEP-1999; 9905-0153070.
PR 13-SEP-1999; 9905-0153758.
PR 15-SEP-1999; 9905-0154018.
PR 16-SEP-1999; 9905-0154039.
PR 20-SEP-1999; 9905-0154779.
PR 22-SEP-1999; 9905-0155139.
PR 23-SEP-1999; 9905-0155486.
PR 24-SEP-1999; 9905-0155659.
PR 28-SEP-1999; 9905-0156458.
PR 29-SEP-1999; 9905-0156596.
PR 04-OCT-1999; 9905-0157117.
PR 05-OCT-1999; 9905-0157753.
PR 06-OCT-1999; 9905-0157865.
PR 07-OCT-1999; 9905-0158029.

```

PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

```

Query Match 55.8%; Score 42.4; DB 21; Length 1395;
Best Local Similarity 72.4%; Pred. No. 0.00049;
Matches 55; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```

```

OY 1 AGTTTCATCAAGACCGCCGATACGGCCATTGGCCGTGACGACCGGACTTCACCTGC 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1175 AGGTTTCAGAAAGACGCGCATGACATTCGGAAGAGACGACCCGACTTCACCTGCG 1234
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 61 GAGGTGTCAGAGCCGC 76
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1235 GAGGTGTCAGAGCCGC 1250
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

```

RESULT 19
AAD22684
ID AAD22684 standard; DNA; 4848 BP.
XX
AC AAD22684;
XX
DT 26-FEB-2002 (first entry)
XX
DE Streptomyces fradiae S-adenosylmethionine (SAM) operon DNA.
XX
KW S-adenosylmethionine; SAM operon; SAM synthetase; methyltransferase;
KW MT; methylene tetrahydrofolate reductase; MTHFR; activated methyl cycle;
KW tylosin production; ds.
XX
OS Streptomyces fradiae.
XX
XX
FH Key Location/Qualifiers
FT 986..2209
FT /*tag= a
FT /product= "SAM synthetase protein"
FT 2241..3341
FT /*tag= b
FT /product= "Methyltransferase protein"
FT /transl_except= (2241..2243, aa:Met)
FT 3338..4255
FT /*tag= c
FT /product= "Methylene tetrahydrofolate reductase protein"
FT /transl_except= (3338..3340, aa:Met)
XX

```

```

PN US6312920-B1.
XX
PD 06-NOV-2001.
XX
PF 22-OCT-1997; 97US-0955957.
XX
PR 13-NOV-1996; 96US-030898P.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Dehoff BS, Rosteck PR;
XX
XX WPI: 2002-024904/03.
DR P-PSDB; AAE13583, AAE13584, AAE13585.
XX
PT New S-adenosylmethionine (SAM) operon from Streptomyces fradiae which
PT encodes SAM synthetase, methyltransferase and methylene
PT tetrahydrofolate reductase, useful for producing SAM by recombinant
PT techniques
XX
PS Claim 19; Column 11-20; 22pp; English.
XX
CC The patent discloses Streptomyces fradiae S-adenosylmethionine (SAM)
CC operon which comprises three genes encoding SAM synthetase, methyl-
CC transferase (MT) and methylene tetrahydrofolate reductase (MTHFR).
CC SAM synthetase, MT and MTHFR together comprise the activated methyl
CC cycle which produces SAM and provides methyl groups required for
CC the final steps in tylosin production. The invention also relates
CC to vectors and transformed heterologous host cells for expressing
CC SAM synthetase. It also relates to a method useful for producing
CC SAM by recombinant techniques. The present DNA sequence is SAM
CC operon from Streptomyces fradiae.
XX
SO Sequence 4848 BP; 648 A; 1869 C; 1696 G; 635 T; 0 other;

```

```

Query Match 50.3%; Score 38.2; DB 24; Length 4848;
Best Local Similarity 78.0%; Pred. No. 0.011;
Matches 46; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

```

```

OY 4 TTTCATCAAGACCGCCGATACGGCCATTGGCCGTGACGACCGGACTTCACCTGCGCA 62
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 2105 TACGCCAAGACCGCCGCTTACGGCCATTCGCGCGCACTGCCGAGTCCGAGTTCACCTGCGCA 2163
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

```

RESULT 20
AAD22686
ID AAD22686 standard; mRNA; 4848 BP.
XX
AC AAD22686;
XX
DT 26-FEB-2002 (first entry)
XX
DE Streptomyces fradiae S-adenosylmethionine (SAM) operon mRNA.
XX
KW S-adenosylmethionine; SAM operon; SAM synthetase; methyltransferase;
KW MT; methylene tetrahydrofolate reductase; MTHFR; activated methyl cycle;
KW tylosin production; ss.
XX
OS Streptomyces fradiae.
XX
XX
FH Key Location/Qualifiers
FT US6312920-B1.
FT 06-NOV-2001.
FT 22-OCT-1997; 97US-0955957.
FT 13-NOV-1996; 96US-030898P.
FT (ELIL ) LILLY & CO ELI.
FT Dehoff BS, Rosteck PR;
FT WPI: 2002-024904/03.
XX

```

xx	The present sequence is used to produce the recombinant DNA compounds of the invention. The specification describes a recombinant DNA compound expressing recombinant polypeptide synthase genes in host cells for the production of narbononide, narbononide derivatives and polyketides that are useful as antibiotics and as intermediates in the synthesis of compounds with pharmaceutical value. The DNA compounds may also encode a C12-hydroxylase (PICK), desosamine biosynthesis and desosaminyl transferase enzymes (useful for conversion of ketolids to antibiotics), and the beta-glucosidase enzyme (involved in picromycin biosyntheseis). These compounds are also useful for increasing the antibiotic activity of a compound relative to the unhydroxylated compound. The recombinant host cells are useful as genetic systems that allow rapid engineering of the narbononide polyketide synthase. These would be valuable for creating novel ketolid analogs for pharmaceutical applications.
SO	Sequence 1693 BP; 237 A; 566 C; 633 G; 257 T; 0 other;
Dy	Query Match 49.5%; Score 37.6; DB 21; Length 1693; Best Local Similarity 76.7%; Pred.No.0.015; Matches 46; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Dz	4 TTCATCAGACCGCCGCACTTGTGGCCGTGCAGGCCGACTTAACCTTCGAG 63 Dz 798 TACTCCAGACCOCGCCCTACGCGCACCTTGCGCGAGCTGCGACTTACCTGGAG 739
RESULT 22	
ID	.AAZ56005/c
AC	.AAZ56005 standard; DNA; 1693 BP.
XX	AAZ56005:
DT	23-MAR-2000 (first entry)
DE	Contig 004 from cosmid PKOS023-27 from Streptomyces venezuelae.
KW	Narbornonide polyketide synthase; PKS; cosmid PKOS023-27; contig 004; ketolide; SAM synthase; S-adenosylmethionine synthase; hydroxylase; picrotoxin; antitubercular production; narbornonin; ds.
OS	Streptomycetes venezuelae.
Key	Location/Qualifiers
CDS	complement (694..1692) /*tag= a /product= SAM_synthase /note= "Partial S-adenosylmethionine synthase" complement (3..692) /*tag= b /product= ORF16-product /note= "M. tuberculosis cbhk homologous partial protein"
MOJ96I599-A2.	
02-DEC-1999.	
27-MAY-1999;	99WO-US11814.
28-MAY-1998;	98US-0087080.
28-AUG-1998;	98US-0141908.
22-SEP-1998;	98US-0100880.
08-FEB-1999;	99US-0119139.
(KOSA-) KOSAN BIOSCIENCES INC.	
Ashley G, Betlach MC, Betlach M, McDaniel R, Tang L;	
WIPI: 2000-072618/06.	
P-PSDB; AAU67216, AAU67217.	
New recombinant DNA encoding a domain of narbornonide polyketide synthase, forproduction of ketolide antibiotics -	

Dislosure; Page 38; 98pp; English.

This is contig 004 from the recombinant cosmid pKOS023-27 DNA sequence (see AA256001) which contains a Streptomyces venezuelae DNA insert. The cosmid contains open reading frames which encode the various modules of the nardoniolide polyketide synthase (PKS). The invention relates to recombinant DNA containing a coding sequence for a nardoniolide PKS. Polyketides are compounds synthesized from 2-carbon units through a series of condensations and subsequent modifications. Modular PKSs are responsible for the production of many antibiotics including plicomycin. The nardoniolide PKS consists of a loading module, six extender modules, and two thioester domains. Four proteins make up the nardoniolide PKS (PICAI, PICAI, PICAI and PICAI). PICAI includes the loading module and extender modules 1 and 2, PICAI includes extender modules 3 and 4, PICAI includes extender module 5 and PICAI includes extender module 6 and a type II thioesterase domain. The second type II thioesterase domain is found on the PICB protein. The nucleotide sequences encoding all of these proteins can be isolated in recombinant form from the recombinant cosmid pKOS023-27. Nardoniolide is desosaminylated in *S. venezuelae* to yield nardomycin, the desosaminyl transferase enzyme is required for this conversion, and the desosamine biosynthetic genes are also found in cosmid pKOS023-27. The recombinant DNA of the invention is used to express, in transformed cells, nardoniolide (or its derivatives) or other ketolides (particularly hybrids), which may then be converted (e.g. by other enzymes recombinantly expressed in the same hosts) to polyketide antibiotics or their intermediates. The antibiotics are useful in human or veterinary medicine.

Sequence 1693 BP; 237 A; 566 C; 633 G; 257 T; 0 other:

Query Match 49.5%; Score 37.6; DB 21; Length 1693;
Best Local Similarity 76.7%; Pred. No. 0.015;
Matches 46; Conservative 0; Mismatches 14; Indels 0; Gaps 0

4 TTCATCAGAGCCGCCGATACGGCCACTTTGGCCCGACGACGCCGACCTTCACCTCGAG 63
Db TATCTCCACGACCGCGCCCTACGCGCACTTGGCCGCGGACCTCGGACCTTCACCTCGAG 739

RESULT 23 -
ID ABL72111 standard; CDNA; 297 BP.
AC ABL72111;
DF 14-MAY-2002 (first entry)
DE Corn tassal-derived polynucleotide (cdps) SFO ID NO:1485.
KM Corn; corn tassal-derived polynucleotide; cdps; hybrid breeding; CDPS;
KW Inheritance; Characteristic; growth; development; disease resistance;
KW environmental adaptability; quality; yield; molecular marker;
KW multigene trait; plant breeding; corn tassal; gene; ss.
OS Zea mays.
XX US2001051335-A1.
XX 13-DEC-2001.
XX 16-APR-1999; 99US-0294093.
XX 21-APR-1998; 98US-082567P.
XX (LALG/) LALGUDI R V.
XX (ITOL/) ITO L Y.
XX (SHER/) SHERMAN B K.
XX Lalgudi RV, Ito LY, Sherman BK;
XX WPI: 2002-163647/21.
XX

```

PT      Novel purified corn tassel-derived polynucleotide useful for
PS      determining altered gene expression, to recover regulatory elements and
XX      to follow inheritance of desirable characteristics through hybrid
XX      breeding programs
PS      Claim 1; SEQ ID 1485; 201pp; English.
XX
CC      The present sequence describes a purified corn tassel-derived
CC      polynucleotide sequence (cdps) comprising a nucleic acid sequence
CC      selected from those given in ABL70627 to ABL76833. The cdps sequences
CC      encode corn tassel-derived polypeptides (CDPS). The cdps sequences (1)
CC      can be used for determining altered gene expression, to recover
CC      regulatory elements and to follow inheritance of desirable
CC      characteristics through hybrid breeding programs. (1) are also useful
CC      in the evaluation, and alteration of desired characteristics associated
CC      with growth and development, disease resistance, environmental
CC      adaptability, quality and yield, and as molecular markers for studying
CC      inheritance of multigenic traits in a plant breeding program. (1) can be
CC      used to produce a tassel-specific profile of gene transcription, a
CC      transcript image, to clone regulatory elements for use in transformation
CC      vectors, to express a polypeptide, to identify, isolate or extend
CC      identical or related corn tassel nucleic acid sequences from DNA
CC      libraries, in nucleic acid hybridisation or amplification technologies,
CC      as query sequences to determine homology of known sequences, as probe
CC      for use in Southern or Northern hybridisation, and to identify the
CC      presence of and/or to determine the degree of similarity between two
CC      (or more) nucleic acid sequences.
XX
SQ      Sequence 297 BP; 58 A; 85 C; 77 G; 50 T; 27 other:
XX
Query Match          49.2%; Score 37.4; DB 24; Length 297;
Best Local Similarity 78.6%; Pred. No. 0.015;
Matches 44; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
OY      2 GGTGATCATCAGACCGCCGATACGGCCACTTGGCGCGTAGACGACGCGGACTTCACC 57
XX      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      242 GCTACTCTCAAGCGCGCGCTTACGGCMACTTTGGAAAGGACGACCCCTGACTTCACC 297
XX
RESULT 24
AA064204
ID      AA064204 standard; cDNA; 1208 BP.
XX
XX      AA064204;
XX
XX      18-NOV-1994 (first entry)
XX
DE      snac gene encoding enzyme in streptogramin biosynthetic pathway.
XX
XX      Antibiotic; streptogramin; snac; snab; snac; biosynthesis; enzyme;
XX      biosynthetic pathway; Streptomyces pristinaespiralis; ds.
XX
XX      Streptomyces pristinaespiralis.
XX
XX      Key Location/Qualifiers
XX      CDS 1..1209
XX      FT /*tag= a
XX
XX      FR2696189-A.
XX
XX      PD 01-APR-1994.
XX
XX      PF 25-SEP-1992; 92FR-0011441.
XX
XX      PR 25-SEP-1992; 92FR-0011441.
XX
XX      (RHON ) RHONE POULENC RORER SA.
XX
XX      Blanc V, Blanche F, Crouzet J, Jacques N, Lacroix P;
XX      Thibaut D, Zagorec M;
XX
XX      WPI. 1994-128286/16.
XX
XX      P-PSDB; AAR54204.
DR

```

XX DNA involved in streptogramin antibiotic biosynthesis - for
PT prodn. or bio-conversion of streptogramin(s) or prodn. of
PT streptogramin intermediates, derivs. or hybrid antibiotics
XX
PS Claim 2: Page 54-55; 83pp; French.
XX
CC The snac gene product is involved in the biosynthesis of
CC streptogramins, antibiotics active against Gram-positive bacteria.
CC The identification of the sequences encoding the enzymes involved
CC in the biosynthetic pathway means that they can be isolated and
CC manipulated. Mutant microorganisms in which a step in the
CC streptogramin biosynthetic pathway is blocked can be cultured to
CC produce streptogramin intermediates, which may later be converted
CC to streptogramin derivatives. Recombinant cells may also be used
CC for the bioconversion of streptogramins from one form to another or
CC for the production of hybrid antibiotics.
XX
SO Sequence 1208 BP; 190 A; 500 C; 360 G; 158 T; 0 other;

Query Match 49.2%; Score 37.4; DB 15; Length 1208;
Best Local Similarity 74.6%; Pred. No. 0.017;
Matches 47; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 13 ACCGCCGATACGCCGACCTTTGGCCGTGACAGCGCGACTTACCTCGCAGGTGTCAG 72
DB 1114 ACCGCCGCTACGCGCCTTGGCCGCGAAGTCCGCGACTTACCTGGAGCGACCGAC 1173
OY 73 CCC 75
DB 1174 CGC 1176

RESULT 25
AA064201
ID AA064201 standard; cDNA; 5392 BP.
XX
AC AA064201;
XX
DT 18-NOV-1994 (first entry)
XX
DE Sequence comprising the snab, snab and snac gene cluster.
XX
KM Antibiotic; streptogramin; snab; snab; snac; biosynthesis; enzyme;
KM biosynthetic pathway; Streptomyces pristinaespiralis; ds.
XX
OS Streptomyces pristinaespiralis.
XX
PN FR2696189-A.
XX
PD 01-APR-1994.
XX
PF 25-SEP-1992; 92FR-0011441.
XX
PR 25-SEP-1992; 92FR-0011441.
XX
PA (RHON) RHONE POULENC RORER SA.
XX
PI Blanc V, Blanche F, Crouzet J, Jacques N, Lacroix P;
PI Thibaut D, Zagorec M;
XX
DR WPI; 1994-128286/16.
XX
XX DNA involved in streptogramin antibiotic biosynthesis - for
PT prodn. or bio-conversion of streptogramin(s) or prodn. of
PT streptogramin intermediates, derivs. or hybrid antibiotics
XX
PS Disclosure; Page 44-47; 83pp; French.
XX
CC This sequence comprises the snab, snab and snac genes which are
CC involved in the biosynthesis of streptogramins, antibiotics active
CC against Gram-positive bacteria. The identification of the sequences
CC encoding the enzymes involved in the biosynthetic pathway means that

CC they can be isolated and manipulated. Mutant microorganisms in
CC which a step in the streptogramin biosynthetic pathway is blocked
CC can be cultured to produce streptogramin intermediates, which may
CC later be converted to streptogramin derivatives. Recombinant cells
CC may also be used for the bioconversion of streptogramins from one
CC form to another or for the production of hybrid antibiotics.
XX
SO Sequence 5392 BP; 811 A; 2161 C; 1671 G; 749 T; 0 other;

Query Match 49.2%; Score 37.4; DB 15; Length 5392;
Best Local Similarity 74.6%; Pred. No. 0.02;
Matches 47; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 13 ACCGCCGATACGCCGACCTTTGGCCGTGACAGCGCGACTTACCTCGCAGGTGTCAG 72
DB 4671 ACCGCCGCTACGCGCCTTGGCCGCGAAGTCCGCGACTTACCTGGAGCGACCGAC 4730
OY 73 CCC 75
DB 4731 CGC 4733

RESULT 26
AA199683
ID AA199683 standard; DNA; 4403765 BP.
XX
AC AA199683;
XX
DT 15-JAN-2002 (first entry)
XX
DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
XX
KM Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
KM variation; epidemiology; patient treatment; epidemic monitoring; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN US6294328-B1.
XX
PD 25-SEP-2001.
XX
PF 24-JUN-1998; 98US-0103840.
XX
PR 24-JUN-1998; 98US-0103840.
XX
PA (GENO-) INST GENOMIC RES.
XX
PI Fleischmann RD, White OR, Fraser CM, Venter JC;
XX
DR WPI; 2001-647261/74.
XX
XX Evaluating strain variation of Mycobacterium tuberculosis, comprises
PT determining the nucleotide sequence of the strain at positions in the
PT genome corresponding to positions where M. tuberculosis strains CDC
PT 1551 and H37Rv differ.
XX
PS Claim 4: SEQ ID NO 2: 3pp + Sequence Listing; English.
XX
XX The invention relates to evaluating strain variation within and between
CC different populations of the tuberculosis bacterial pathogen,
CC Mycobacterium tuberculosis or related Mycobacterium by determining the
CC nucleotide sequence of the first strain at positions in the complete
CC sequence of the genome that correspond to positions that differ in the
CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and
CC H37Rv (AA199682). The method is useful for evaluating strain variation of
CC M. tuberculosis and has valuable application in the fields of
CC tuberculosis genetics, epidemiology, patient treatment and epidemic
CC monitoring.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?docID=6294328B1.
XX
SO Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;

Query Match 45.3%; Score 34.4; DB 22; Length 4403765;
Best Local Similarity 73.3%; Pred. No. 0.31;
Matches 44; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 12 GACCGCGCATAGCGCACTTGGCCGTGACGACGCCGACTTCACCTCGGAGGTGCTCAA 71
Db 1567783 GACCGCGCGCTAGCGCACTTGGCCGTGACGACGCCGACTTCACCTCGGAGGTGCTCAA 1567842

RESULT 27
AA199682
ID AA199682 standard; DNA: 4411529 BP.
AC AA199682;
XX
DT 15-JAN-2002 (first entry)
XX
DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
XX
KM Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
KW variation; epidemiology; patient treatment; epidemic monitoring; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN US6294328-B1.
XX
PD 25-SEP-2001.
XX
PF 24-JUN-1998; 98US-0103840.
XX
PR 24-JUN-1998; 98US-0103840.
XX
PA (GENO-) INST GENOMIC RES.
XX
PI Fleischmann RD, White OR, Fraser CM, Venter JC;
DR WPI: 2001-647261/74.
XX
PT Evaluating strain variation of Mycobacterium tuberculosis, comprises
PT determining the nucleotide sequence of the strain at positions in the
PT genome corresponding to positions where M. tuberculosis strains CDC
PT 1551 and H37Rv differ
XX
PS Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.
XX
CC The invention relates to evaluating strain variation within and between
CC different populations of the tuberculosis bacterial pathogen,
CC Mycobacterium tuberculosis or related Mycobacterium by determining the
CC nucleotide sequence of the first strain at positions in the complete
CC sequence of the genome that correspond to positions that differ in the
CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and
CC H37Rv (AA199682). The method is useful for evaluating strain variation of
CC M. tuberculosis and has valuable application in the fields of
CC tuberculosis genetics, epidemiology, patient treatment and epidemic
CC monitoring.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?docid=6294328B1.
XX
SQ Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;

Query Match 45.3%; Score 34.4; DB 22; Length 4411529;
Best Local Similarity 73.3%; Pred. No. 0.31;
Matches 44; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 12 GACCGCGCATAGCGCACTTGGCCGTGACGACGCCGACTTCACCTCGGAGGTGCTCAA 71
Db 1567944 GACCGCGCGCTAGCGCACTTGGCCGTGACGACGCCGACTTCACCTCGGAGGTGCTCAA 1568003

RESULT 28
AAA81476

ID AAA81476 standard; DNA: 56485 BP.
XX
XX AAA81476;
AC
XX
DT 04-DEC-2000 (first entry)
XX
XX N. meningitidis partial DNA sequence gnm_24 SEQ ID NO:24.
DE
XX
KM Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW Meningococcus B; MenB; ds.
XX
OS Neisseria meningitidis.
XX
PN WO200022430-A2.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-US23573.
XX
PR 09-OCT-1998; 98US-0103794.
PR 30-APR-1999; 99US-0132068.
XX
PA (CHIR) GIRON CORP.
XX
PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Pizza M;
DR WPI: 2000-318079/27.
XX
PT Isolated nucleotide sequences of Neisseria meningitidis which can be
PT used in the diagnosis and treatment of N. meningitidis infection and
PT other Neisseria infections, for example, N.gonorrhoea
XX
PS Claim 7; Page 507-524; 1760pp; English.
XX
XX The present invention describes methods of obtaining immunogenic
CC proteins from Neisseria genomic sequences. AAA81453 to AAA82414
CC represent specifically claimed Neisseria meningitidis genomic DNA
CC sequences. AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to
CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
CC isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
CC AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC sequences, which are all used in the exemplification of the present
CC invention. The nucleic acid sequences, protein sequences, and antibodies
CC against them, can be used in the manufacture of a composition. The
CC composition can be used as a medicament (or in the manufacture of a
CC medicament) for treating, preventing or diagnosing infection due to
CC Neisseria bacteria. For example, some of the identified proteins could
CC be components of vaccines against Meningococcus B; against all serotypes;
CC and/or against all pathogenic Neisseriae. Identification of sequences
CC from the bacterium will also facilitate production of biological probes,
CC particularly organism-specific probes. Attempts to make efficacious
CC Meningococcus B vaccines have failed mainly due to antigen tolerance.
CC Multivalent vaccines have also been tried but none have successfully
CC overcome antigenic variability. The provision of further, complete
CC sequences may provide an opportunity to identify secreted or surface
CC exposed proteins that may be presumed targets for the immune system and
CC which are not antigenically variable or at least more conserved than
CC other more variable regions.
XX
SQ Sequence 56485 BP; 12504 A; 14247 C; 16158 G; 13573 T; 3 other;

Query Match 43.2%; Score 32.8; DB 21; Length 56485;
Best Local Similarity 71.7%; Pred. No. 0.67;
Matches 43; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 4 TTCACTAAGACCGCGCATAGCGCACTTGGCCGTGACGACGCCGACTTCACCTCGGAG 63
Db 54065 TACACTAATCCCGCGCTTACGACACTTTCGCGCGGAGAACCTGACTTCGGAG 54124

```
RESULT 29
AAAF21612/C
ID   AAAF21612 standard; DNA; 349980 BP.
XX
AC   AAAF21612;
XX
DT   13-MAR-2001 (first entry)
XX
DE   Neisseria meningitidis B nucleotide sequence SEQ ID NO:113.
XX
KW   Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
KM   diagnosis; antigen; detection; infection; gene therapy; antibacterial;
XX   ds.
OS   Neisseria meningitidis.
XX
PN   WO20006791-A1.
XX
PD   09-NOV-2000.
XX
PF   08-MAR-2000; 2000MO-US05928.
XX
PR   30-APR-1999; 99US-0132068.
PR   08-OCT-1999; 99MO-US23573.
PR   28-FEB-2000; 2000GB-0004695.
XX
PA   (CHIR ) CHIRON CORP.
PA   (GENO-) INST GENOMIC RES.
XX
PI   Pizze M, Hickey E, Peterson J, Tettelin H, Venter JC, Masignani V,
PI   Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V, Rappuoli R;
PI   Frazer CM, Grandi G;
XX
DR   WPI: 2000-647603/62.
XX
PT   Neisseria meningitidis B full length genome sequence and open reading
PT   frames are used to detect, treat and prevent Neisserial infections -
XX
PS   Claim 7; Appendix A; 692pp; English.
XX
CC   The present invention describes the full length genome of
CC   Neisseria meningitidis B (NMB). The sequences in AAAF21544 and AAAF21607
CC   to AAAF21613 represent fragments of the NMB genomic sequence, as the
CC   sequence was too long to go in a record on its own it was split into 8
CC   sequences which overlap each other at the beginning and end of each
CC   sequence by 49980 bp (i.e. the last 49980 bp of AAAF21544 is repeated at
CC   the beginning of AAAF21607, the last 49980 bp of AAAF21607 are repeated at
CC   the beginning of AAAF21608, and so on). AAAF21545 to AAAF21588 encode the
CC   Neisseria proteins given in AAB58550 to AAB58593, and AAAF21589 to
CC   AAAF21606 represent PCR primers which are used in the exemplification of
CC   the present invention. The NMB genome and fragments from it have
CC   antibacterial activity, and can be used in vaccines and gene therapy.
CC   Neisseria nucleic acids, proteins and/or antibodies which binds to the
CC   proteins can be used in compositions for treating or preventing infection
CC   due to Neisserial bacteria or as a diagnostic reagent for detecting the
CC   presence of Neisserial bacteria or of antibodies raised to Neisserial
CC   bacteria. Computers, computer memory, computer storage medium or computer
CC   databases can be used in a search to identify open reading frames (ORFs)
CC   or coding sequences within the NMB genome. The DNA sequences provide
CC   further opportunities to find antigenic or immunogenic proteins which are
CC   more effective in vaccines than the outer membrane proteins currently
CC   used.
XX
SQ   Sequence 349980 BP; 86473 A; 95646 C; 85908 G; 81953 T; 0 other;
XX
```

```
Query Match          43.2%; Score 32.8; DB 21: Length 349980;
Best Local Similarity 71.7%; Pred. No. 0.79;
Matches 43; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
```

```
0Y 4 TTTCATCAAGACCGCGCATCTTGCGCGACGACGACGACGACGACGACGAG 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87588 TACAGTAAATCCGCCGCTTACGACATTTTGGCCCGGAGAACTGAGTTCACTTGGAG 87530
```

```
RESULT 30
AAA81489/C
ID   AAA81489 standard; DNA; 837096 BP.
XX
AC   AAA81489;
XX
DT   04-DEC-2000 (first entry)
XX
DE   N. meningitidis partial DNA sequence gnm_37 SEQ ID NO:37.
XX
KW   Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
KM   antigen; vaccine; diagnosis; infection; antibacterial; identification;
XX   Meningococcus B; MenB; ds.
XX
OS   Neisseria meningitidis.
XX
PN   WO200022430-A2.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999; 99MO-US23573.
XX
PR   09-OCT-1998; 98US-0103794.
PR   30-APR-1999; 99US-0132068.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC,
PI   Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V,
PI   Rappuoli R, Pizze M;
XX
DR   WPI: 2000-318079/27.
XX
PT   Isolated nucleotide sequences of Neisseria meningitidis which can be
PT   used in the diagnosis and treatment of N. meningitidis infection and
PT   other Neisserial infections, for example, N.gonorrhoea -
XX
PS   Claim 7; Page 629-865; 1760pp; English.
XX
CC   The present invention describes methods of obtaining immunogenic
CC   proteins from Neisseria genomic sequences. AAA81453 to AAA82414
CC   represent specifically claimed Neisseria meningitidis genomic DNA
CC   sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
CC   Neisseria DNA sequences and their corresponding proteins; AAA81254 to
CC   AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
CC   isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
CC   AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC   sequences, which are all used in the exemplification of the present
CC   invention. The nucleic acid sequences, protein sequences, and antibodies
CC   against them, can be used in the manufacture of a composition. The
CC   composition can be used as a medicament (or in the manufacture of a
CC   medicament) for treating, preventing or diagnosing infection due to
CC   Neisserial bacteria. For example, some of the identified proteins could
CC   be components of vaccines against Meningococcus B; against all serotypes;
CC   and/or against all pathogenic Neisseriae. Identification of sequences
CC   from the bacterium will also facilitate production of biological probes,
CC   particularly organism-specific probes. Attempts to make efficacious
CC   Meningococcus B vaccines have failed mainly due to antigen tolerance.
CC   Multivalent vaccines have also been tried but none have successfully
CC   overcome antigenic variability. The provision of further, complete
CC   sequences may provide an opportunity to identify secreted or surface
CC   exposed proteins that may be presumed targets for the immune system and
CC   which are not antigenically variable or at least more conserved than
CC   other more variable regions.
XX
SQ   Sequence 837096 BP; 207534 A; 227065 C; 205215 G; 197280 T; 2 other;
XX
```

```
Query Match          43.2%; Score 32.8; DB 21: Length 837096;
Best Local Similarity 71.7%; Pred. No. 0.85;
Matches 43; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
```


SQ Sequence 657 BP; 155 A; 175 C; 134 G; 193 T; 0 other;
 Query Match 37.6%; Score 28.6; DB 21; Length 657;
 Best Local Similarity 61.3%; Pred. No. 9;
 Matches 46; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 OY 1 AGGTCATCAAGACCGCCGATACGCTTGGCCGACGACGCGACTTCACCTGC 60
 DB 221 ATGGCGCATTCAGACGACGCCAAATGCGAGTTGCTTATGACTACGTCGAGATTACCCGC 280
 OY 61 GAGGTGCTCAAGCCC 75
 DB 281 GACGTGATCAGTGC 295
 RESULT 33
 AAF08609
 ID AAF08609 standard; cDNA; 383 BP.
 AC AAF08609;
 XX 13-MAR-2001 (first entry)
 DT Fusarium venenatum EST SEQ ID NO:1132.
 DE Fusarium venenatum
 XX Multiple gene expression; filamentous fungal cell; EST;
 KM expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 KM Aspergillus oryzae; Trichoderma reesei; identification; recombination;
 KM culture condition; environmental stress; spore morphogenesis;
 KM metabolic pathway engineering; catabolic pathway engineering; ss.
 XX
 OS Fusarium venenatum.
 XX WO200056762-A2.
 PN 28-SEP-2000.
 PD 22-MAR-2000; 2000MO-US07781.
 XX
 PF 22-MAR-1999; 9905-0273623.
 PR (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
 PI MPI, 2000-594572/56.
 DR Monitoring differential expression of genes in filamentous fungal cells
 XX PT uses fluorescence-labeled nucleic acids isolated from the cells and a
 PT substrate of expressed sequence tags -
 XX
 PS Claim 86; Page 813; 3161pp; English.
 CC The present invention describes a method for monitoring differential
 CC expression of genes in a first filamentous fungal (FF) cell relative to
 CC expression of the same genes in one or more second filamentous fungal
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 CC are used in the methods for monitoring differential expression of genes
 CC in a first filamentous fungal (FF) cell relative to expression of the
 CC same genes in one or more second filamentous fungal cells. Monitoring
 CC the global expression of genes from FF cells allows the production
 CC potential of the microorganisms to be improved. New genes may be
 CC discovered, possible functions of unknown open reading frames can be
 CC identified and gene copy number variation and stability can be
 CC monitored. The expression of genes can be used to study how FF cells
 CC adapt to changes in culture conditions, environmental stress, spore
 CC morphogenesis, recombination, metabolic or catabolic pathway
 CC engineering. Using ESTs provides several advantages over genomic or
 CC random cDNA clones including elimination of redundancy as one spot on an
 CC array equals one gene or open reading frame, and organisation of the
 CC microarrays based on function of the gene products to facilitate

CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
 CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
 CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
 CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
 CC all specifically claimed in the present invention.
 XX
 SQ Sequence 383 BP; 74 A; 115 C; 87 G; 89 T; 18 other;
 Query Match 36.6%; Score 27.8; DB 21; Length 383;
 Best Local Similarity 61.1%; Pred. No. 15;
 Matches 44; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
 OY 4 TTCATCAAGACCGCCGATACGCGCCGTCGACGACGCGGACTTCACCTGCAG 63
 DB 145 TACTTTGAGAACCTGCTCTGTCTGCTGCTGCGCGCGCGCGCGCCAGAC 204
 OY 64 GGTGTCAGGCC 75
 DB 205 TTCTTCATTCCTC 216
 RESULT 34
 ABK13571
 ID ABK13571 standard; cDNA; 2284 BP.
 AC ABK13571;
 XX 23-APR-2002 (first entry)
 DT Ryegrass 4-coumarate Co-A-lyase 1 (Lp4CL1) cDNA.
 DE Ryegrass 4-coumarate Co-A-lyase 1 (Lp4CL1) cDNA.
 XX
 KM Perennial ryegrass; ss; lignin; 4 coumarate CoA-lyase; QTL; gene;
 KM lignin biosynthesis; enzyme; cinamoyl-CoA reductase; CCR; Lp4CL1;
 KM cinamoyl alcohol dehydrogenase; CAD; molecular genetic marker;
 KM qualitative trait loci; tagging; QTL mapping; DNA fingerprinting;
 KM marker assisted selection; forage improvement; turf grass improvement;
 KM dry matter digestibility; herbage quality; palatability; regrowth;
 KM cold tolerance; drought tolerance; tiller survival; plant persistence.
 XX
 OS Lolium perenne.
 XX
 FH Key Location/Qualifiers
 FT 1..322
 FT 5'UTR
 FT /tag= a
 FT CDS 323..2146
 FT /tag= b
 FT /product= "Lp4CL1 protein"
 FT /transl_except= (pos:2030..2038, aa:Ala Arg)
 FT 3'UTR 2147..2266
 FT /tag= c
 FT polyA_site 2267..2284
 FT /tag= d
 XX
 PN WO200195702-A1.
 PD 20-DEC-2001.
 XX 14-JUN-2001; 2001WO-AU00699.
 PF 14-JUN-2000; 2000AU-0008154.
 PR (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
 PA (UVAD-) UNIV ADELAIDE.
 PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
 PA (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
 PA (UVSC-) UNIV SOUTHERN CROSS.
 PA (DAIR-) DAIRY RES & DEV CORP.
 XX Spangenberg GC, Lidgett AJ, Heath RL, McInnes RL, Lynch DP;
 PI MPI, 2002-097993/13.
 DR P-PSDB; AAU75084.
 XX

PT Novel nucleic acid encoding enzymes involved in lignin biosynthetic
PT pathway from ryegrass or fescue species useful for modifying lignin
PT biosynthesis in plants and as a molecular genetic marker
XX
PS Claim 3; Fig 2; 148bp; English.
XX
CC This invention represents purified or isolated nucleic acid and protein
CC sequences of enzymes involved in lignin biosynthesis. The enzymes
CC of the invention are 4 coumarate CoA-lyase (4CL), cinnamoyl-CoA
CC reductase (CCR) and cinnamyl alcohol dehydrogenase (CAD) from a ryegrass
CC (Lolium sp.) or fescue (Festuca sp.). The invention also comprises an
CC isolated regulatory element from the nucleic acid sequences and a plant
CC cell or seed transformed with the nucleic acid. An isolated regulatory
CC element from these nucleotide molecules is useful for expressing an
CC exogenous gene in plant cells. The nucleotide sequences of the invention
CC and vectors containing these sequences are useful for modifying lignin
CC biosynthesis in a plant and are useful as a molecular genetic marker for
CC qualitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting,
CC and in marker assisted selection, in forage and turf grass improvement,
CC e.g. tagging QTLs for dry matter digestibility, herbage quality,
CC palatability, regrowth after cutting and grazing, cold tolerance,
CC drought tolerance, tiller survival and plant persistence. The present
CC sequence represents the perennial ryegrass 4-coumarate Co-A-lyase 1
CC (LP4CL1) cDNA of the invention.
XX
SQ Sequence 2284 BP; 391 A; 750 C; 733 G; 410 T; 0 other:
Query Match 36.6%; Score 27.8; DB 24; Length 2284;
Best Local Similarity 62.0%; Pred. No. 18;
Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 2 GGTTCATCAGACCGCCGATACGCGCCTTTGGCCGTGACGACGCGACTTTCACCTGCG 61
DB 1647 GGTGGCTCCACACGCGGACATCGCTACGTCGACGACGACGAGCTTTCATCGCG 1706
QY 62 AGGTGTCACG 72
DB 1707 ACCGCGTCACG 1717
RESULT 35
AA13227
ID AA13227 standard; DNA; 3600 BP.
XX
AC AA13227;
XX
DT 16-SEP-1996 (first entry)
XX
DE Thermostable enzyme (converting maltose to trehalose) DNA.
XX
KM Thermostable enzyme; thermophilic bacterium; sweetener; trehalose;
KM maltose; food; recombinant enzyme; cosmetic; pharmaceutical; ds.
XX
OS Thermus aquaticus ATCC 33923.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..540
FT /tag= a
FT mat_peptide 541..3429
FT /tag= b
FT 3'UTR 3430..3600
FT /tag= c
XX
PN EP04531-A2.
XX
PD 03-APR-1996.
XX
PF 29-SEP-1995; 95EP-0306875.
XX
PR 08-SEP-1995; 95JP-0255829.
PR 01-OCT-1994; 94JP-0260984.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX
PI Kubota M, Sugimoto T, Tsusaki K;
XX
DR WPI: 1996-173035/18.
XX
DR P-PSDB: AAR84081, AAR84082.
XX
PT Isolated DNA encoding enzyme for converting maltose to trehalose
PT used for prodn. of trehalose for use in food prods., cosmetics and
PT pharmaceuticals, partic. as sweetener
XX
PS Claim 8; Page 28-31; 46pp; English.
XX
CC This DNA encoding a thermostable enzyme which converts maltose to
CC trehalose may be used to express the enzyme recombinantly in E. coli
CC using plasmid vector Bluescript II SK(+) or plasmid pK223-3. The
CC enzyme is then produced by culturing the transformant. The enzyme
CC catalyses a reaction to produce high yields of trehalose at high
CC temp., which prevents bacterial contamination. Trehalose is used in
CC food products, cosmetics and pharmaceuticals, as a sweetener, etc.
XX
SQ Sequence 3600 BP; 559 A; 1346 C; 1168 G; 527 T; 0 other:
Query Match 36.6%; Score 27.8; DB 17; Length 3600;
Best Local Similarity 62.0%; Pred. No. 19;
Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 2 GGTTCATCAGACCGCCGATACGCGCCTTTGGCCGTGACGACGCGACTTTCACCTGCG 61
DB 1412 GGATCCCGGAACCGCCGATGCGCCCTTCTCCGACACGACGAGCTCACCTCGG 1471
QY 62 AGGTGTCACG 72
DB 1472 AGAAGTCACG 1482
RESULT 36
AA19362
ID AA19362 standard; DNA; 7584 BP.
XX
AC AA19362;
XX
DT 19-MAY-1999 (first entry)
XX
DE Rhodococcus corallina ohp operon.
XX
KM Rhodococcus corallina: ohp operon; biosensor; mycolic acid bacteria;
KM inducible promoter; environmental pollutant; industry; medicine; ds.
XX
OS Rhodococcus corallina.
XX
PN WO9900517-A2.
XX
PD 07-JAN-1999.
XX
PF 29-JUN-1998; 98WO-GB01893.
XX
PR 27-JUN-1997; 97GB-0013666.
XX
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI Archer JAC, Powell JAC, Roland HJ, Summers DK;
XX
DR WPI: 1999-095760/08.
DR P-PSDB: AAW9181, AAW9182, AAW9183, AAW9184, AAW9185, AAW9186.
XX
PT Isolating DNA encoding inducible promoter from mycolic acid bacteria
PT - useful to produce mycolic acid bacterial biosensors for particular
PT analyses, such as environmental pollutants, e.g. from industry or
PT medicine
XX
PS Example 7; Fig 4; 67pp; English.
XX
A method has been developed for identifying and/or isolating DNA from

CC mycolic acid bacteria which encodes an inducible promoter induced in
CC response to a particular analyte (and/or associated operon proteins).
CC The method comprises: (a) culturing source of mycolic acid bacteria in
CC specific media containing specific analyte and selective for
CC oligotrophic bacteria; (b) identifying mycolic acid bacteria subsisting
CC on medium; (c) extracting DNA from these bacteria; (d) incorporating DNA
CC into vector; (e) cloning vector into suitable host cell; and (f)
CC screening host cells for inducible promoter and/or proteins to identify
CC vectors encoding it. The method allows isolation of DNA encoding a
CC promoter which is induced in response to a particular analyte (and/or
CC associated operon proteins), which can be used to produce biosensors for
CC the analyte. The DNA is incorporated into vectors which are used to
CC transform host cells to produce the biosensors. It is especially useful
CC when the analyte is an environmental pollutant (e.g. from industry or
CC medicine), especially a hydrophobic organic compound such as components of
CC fuels, pesticides; the biosensors may then be used to detect small
CC concentrations of analytes in samples e.g. for pollution monitoring. The
CC identified DNA can also be modified to produce modified inducible
CC promoters and/or operons also useful in biosensor production. The method
CC allows rapid isolation of promoters (and/or operon proteins) whilst
CC minimising host restrictions (e.g. thick cell walls of mycolic acid
CC bacteria which confer resistance to cell lysis) and requiring no
CC knowledge of inducible enzyme chemistry involved (which may be unknown
CC for specific analyte). The present sequence represents the R. corallina
CC ohp operon, given in the present invention.

XX Sequence 7584 BP; 1329 A; 2735 C; 2286 G; 1234 T; 0 other;

Query Match 36.6%; Score 27.8; DB 20; Length 7584;
Best Local Similarity 69.1%; Pred. No. 20;
Matches 38; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 15 CGCGCATACGGCCACTTGGCCGTGACGACGCCGACTTCACCTGGAGGTGTC 69
DB 5804 CGCGCATTCGACACGACGCCGCGGTTGTCGCGGACTTCGCCCGCATCTATC 5858

RESULT 37
AAAS1878
ID AAAS1878 standard; DNA: 7600 BP.

AC AAAS1878;

XX 31-OCT-2000 (first entry)

DE Rhodococcus sp. OHP operon.

XX OHP operon: orthohydroxyphenylpropionic acid: regulator; inducible;

KM gene expression system; plant transformation; ds.

XX Rhodococcus sp. V49.

OS Rhodococcus sp. V49.

XX Key Location/Qualifiers

FT CDS 296..1036

FT /tag= a

FT /product= ohpH_regulator

FT CDS 1262..2806

FT /tag= b

FT /product= ohpA_transport_protein

FT CDS 2808

FT /tag= c

FT /tag= d

FT /product= ohpB_monooxygenase

FT CDS 5722..6666

FT /tag= e

FT /product= ohpD_catechol_2,3-dioxygenase

XX WO200039300-A1.

PN 06-JUL-2000.

XX 21-DEC-1999; 99WO-GB04333.

XX 24-DEC-1998; 98GB-0028660.

XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.

XX Tuerck JA, Archer JAC;

XX WPI: 2000-452398/39.

XX P-PSDB; AAY97050, AAY97051, AAY97052, AAY97053.

XX New chimeric gene for controlling eukaryotic gene expression or

XX transforming plant tissue of monocot or a dicot crops, trees or other

XX plants, comprises regulatory regions for a regulator polypeptide and a

XX nucleic acid

XX Claim 30; Page 91-100; 114pp; English.

XX This is the OHP (orthohydroxyphenylpropionic acid) operon from

XX Rhodococcus sp. V49. The OHP responsive regulator polypeptide coding

XX sequence can be used in novel chimeric genes for use in chemically

XX inducible gene expression systems. The chimeric gene comprises a

XX promoter and a regulator polypeptide coding sequence linked with a

XX second sequence comprising a promoter and a coding or non-coding

XX sequence. Expression of the target gene of the second sequence is

XX controlled by the regulatory polypeptide which is acted upon by an

XX inducer. The chimeric gene is used to control eukaryotic gene

XX expression or transform plant tissue of monocot or a dicot crops, trees

XX or other plants, such as potato, wheat, barley, tomato, rice,

XX canola, sugarbeet, tobacco, eucalyptus, populus, malus, or Arabidopsis.

XX Carbon metabolism, flowering, fertility and/or sterility, cell wall

XX metabolism, genes that respond to environmental signals, such as pathogen

XX attack, bacterium, fungus, virus, or insect resistance, or genes that

XX confer resistance to antibiotics, herbicides or other toxic compounds can

XX be controlled (all claimed).

XX Sequence 7600 BP; 1332 A; 2742 C; 2289 G; 1237 T; 0 other;

XX Query Match 36.6%; Score 27.8; DB 21; Length 7600;

XX Best Local Similarity 69.1%; Pred. No. 20;

XX Matches 38; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 15 CGCGCATACGGCCACTTGGCCGTGACGACGCCGACTTCACCTGGAGGTGTC 69

DB 5805 CGCGCATTCGACACGACGCCGCGGTTGTCGCGGACTTCGCCCGCATCTATC 5859

RESULT 38

AAAD07974

AD07974 standard; cDNA: 1957 BP.

XX AD07974;

XX 06-AUG-2001 (first entry)

XX Rice cysteinyl-tRNA synthetase cDNA clone rs11n.pk016.p18.

XX Rice; cysteinyl-tRNA synthetase; herbicide; genetic mapping;

XX plant breeding; ss.

XX Oryza sativa.

XX Key Location/Qualifiers

FT CDS 3..1649

FT /tag= a

FT /product= "Cysteinyl-tRNA synthetase"

FT /note= "CDS does not include start codon"

FT /partial

XX US6255090-B1.

XX 03-JUL-2001.

XX 14-JUL-1999; 99US-0352990.


```

XX 15-JUL-1998; 98US-0092866.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Famodu LO, Orozco EM, Rafalski JA;
XX
XX WPI: 2001-3388927/41.
XX P-PSDB: AAE03590.
XX
XX New isolated polynucleotide encoding an aspartyl-LRNA synthetase useful
XX as targets to facilitate design and/or identification of inhibitors of
XX those enzymes that may be useful as herbicides -
XX
XX Example 4; Column 39-42; 40pp; English.
XX
XX The present sequence is a cDNA encoding rice cysteinyl-LRNA synthetase
XX of the invention. The cysteinyl-LRNA synthetase are used as targets to
XX facilitate designing and identification of inhibitors of the enzymes
XX which are useful as herbicides. All or a substantial portion of the
XX nucleic acid fragments of the present invention are used as probes for
XX genetically and physically mapping the genes that they are a part of,
XX and as markers for traits linked to those genes. Such information is
XX useful in plant breeding in order to develop lines with desired
XX phenotypes.
XX
XX Sequence 1957 BP; 599 A; 384 C; 470 G; 504 T; 0 other:
XX
XX Query Match 36.3%; Score 27.6; DB 22; Length 1957;
XX Best Local Similarity 63.6%; Pred. No. 20;
XX Matches 42; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
XX
OY 6 CATCAAGCCGCCGATGCGCATTTGGCGGAGACGCGGACTGACCTGGAGGT 65
DB 176 GGTACGCGCTACGACTTCAGCAGATCGCCAGCGCCGCGCTACGCTGAGGT 235
OY 66 GGTCAA 71
DB 236 CCTCTA 241
XX
XX RESULT 39
XX ABQ90584
XX ID ABQ90584 standard; DNA; 2907 BP.
XX
XX AC ABQ90584;
XX
XX DT 01-OCT-2002 (first entry)
XX
XX DE M. capsulatus gene #569 for DNA array.
XX
XX KW Micro array; gene; ds; differential expression; gene expression.
XX
XX OS Methylococcus capsulatus.
XX
XX PN WO200255655-A2.
XX
XX PD 18-JUL-2002.
XX
XX PF 14-JAN-2002; 2002WO-NO00019.
XX
XX PR 12-JAN-2001; 2001NO-0000235.
XX
XX PR 12-JAN-2001; 2001NO-0000239.
XX
XX PA (UNIT-) UNIFOB STITTELSSEN UNIV BERGEN.
XX (TIGR-) TIGR.
XX
XX Birkeland NK, Bidhammer I, Jonassen I, Jensen HB, Lien T;
XX Lillehaug JR, Lossius I, Eisen JA, Fraser CM, Durkin AS;
XX Salzberg SL;
XX WPI: 2002-557818/59.
XX

```

```

XX Novel DNA array useful for determining differential expression of
XX Methylococcus capsulatus genes, comprises polynucleotides or
XX oligonucleotides representative for a selective number of Methylococcus
XX capsulatus genes -
XX
XX Claim 14; Page 296-297; 678pp; English.
XX
XX The invention relates to a novel DNA array giving a representation of a
XX number of Methylococcus capsulatus genes. The method of the invention is
XX useful for determination of the differential expression of the genes of
XX M. capsulatus, and for studying gene expression on a genomic scale and in
XX gene expression assays of M. capsulatus genes. The sequences shown in
XX ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
XX invention.
XX
XX Sequence 2907 BP; 504 A; 975 C; 887 G; 541 T; 0 other:
XX
XX Query Match 36.3%; Score 27.6; DB 24; Length 2907;
XX Best Local Similarity 60.8%; Pred. No. 21;
XX Matches 45; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
XX
OY 3 GTTCATCAAGACCGCCGATACGCGCACTTTGGCCGTAGACGACGCCGACTTCACCTGCGA 62
DB 915 GTTCACATGATCGCCACCAATGCGACATGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 974
OY 63 GGTCGCAAGCCGCC 76
DB 975 CGCGAGAAACGCC 988
XX
XX RESULT 40
XX AA225727
XX ID AA225727 standard; cDNA; 1791 BP.
XX
XX AC AA225727;
XX
XX DT 05-JAN-2000 (first entry)
XX
XX DE Stachybotrys chartarum phenol oxidising enzyme encoding cDNA.
XX
XX KW Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
XX detergent; anti-dye transfer; stain removal; bleaching; ss.
XX
XX OS Stachybotrys chartarum.
XX
XX PN WO9949010-A2.
XX
XX PD 30-SEP-1999.
XX
XX PF 23-MAR-1999; 99WO-EP02042.
XX
XX PR 24-MAR-1998; 98US-0046969.
XX
XX PR 22-DEC-1998; 98US-0218702.
XX
XX PA (UNIT ) UNILEVER NV.
XX (UNIT ) UNILEVER PLC.
XX
XX Convents D, Amory A, Wang H, Dhaese P, Lambrechts-Rongvaux A;
XX Wang C;
XX WPI: 1999-601211/51.
XX
XX DR P-PSDB: AA45222.
XX
XX PT Detergent composition containing phenol oxidase from Stachybotrys, used
XX to bleach stains and prevent dye transfer -
XX
XX Example 15; Fig 5; 56pp; English.
XX
XX The present invention describes a detergent composition containing a
XX purified phenol oxidising enzyme derived from Stachybotrys. The present
XX sequence encodes Stachybotrys chartarum phenol oxidising enzyme. The
XX enzyme can be used to modify the colour of dyes and other coloured
XX

```

CC compounds (e.g. for use in pulp and paper bleaching also for removing
CC stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye
CC transfer during fabric washing.

XX Sequence 1791 BP; 380 A; 554 C; 448 G; 409 T; 0 other;

Query Match

Best Local Similarity 36.1%; Score 27.4; DB 20; Length 1791;

Matches 43; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

OY 4 TTCATCAGACGCCGACATGCGCCACTTTGGCCGTGACGCGCGACTTCACTGCGAG 63
DB 577 TTCATCAGACGCTGAGATGCTTGTGTCAGCGCTGCGCTACATTATCAACGAC 636
OY 64 GTGCTCAAG 72
DB 637 GAGCGTGAG 645

RESULT 41

AAZ27601
ID AAZ27601 standard; DNA; 1791 BP.

XX AAZ27601;

DI 16-DEC-1999 (first entry)

DE Stachybotrys phenol oxidase coding sequence.

KW phenol oxidase; enzyme; coloured compound; dye transfer prevention;
KM fabric washing; stain bleaching; anti-dye transfer; detergent; ss.

XX Stachybotrys chartarum.

XX WO9949020-A2.

XX 30-SEP-1999.

XX 23-MAR-1999; 99WO-US06327.

XX 24-MAR-1998; 98US-0046969.

XX 22-DEC-1998; 98US-0218702.

XX 22-MAR-1999; 99US-0273957.

XX (GENEV) GENENCOR INT INC.

XX Amory A, Wang H, Dhase P, Lambrechts-Rongvaux A, Wang C;

XX WPI: 1999-591088/50.

XX P-PSDB: AAY39992.

XX Novel enzyme for modifying coloured compounds used to prevent
XX dye-transfer.

XX Claim 21; Fig 5; 64pp; English.

CC This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
CC of the invention. The invention is used to modify a coloured compound and
CC prevent dye transfer during fabric washing, or for stain bleaching or
CC anti-dye transfer. It is useful in the detergent, paper and pulp, textile
CC and food industries.

XX Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;

Query Match

Best Local Similarity 36.1%; Score 27.4; DB 20; Length 1791;

Matches 43; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

OY 4 TTCATCAGACGCCGACATGCGCCACTTTGGCCGTGACGCGCGACTTCACTGCGAG 63
DB 577 TTCATCAGACGCTGAGATGCTTGTGTCAGCGCTGCGCTACATTATCAACGAC 636
OY 64 GTGCTCAAG 72

DB 637 GAGCGTGAG 645

RESULT 42

AA50019
ID AA50019 standard; DNA; 1791 BP.

XX AA50019;

DI 10-OCT-2000 (first entry)

DE Stachybotrys chartarum phenol oxidising enzyme cDNA.

XX phenol oxidising enzyme; detergent; bleaching; ss.

XX Stachybotrys chartarum.

XX Key Location/Qualifiers

XX CDS 7..1791

XX WO200039306-A2.

XX 06-JUL-2000.

XX 20-DEC-1999; 99WO-EPI0287.

XX 23-DEC-1998; 98US-0220871.

XX 23-JUN-1999; 99US-0338723.

XX (UNIL) UNILEVER NV.

XX (UNIL) UNILEVER PLC.

XX (HIND) HINDUSTAN LEVER LTD.

XX Bodie EA, Van Der Velden S, De Vries CH, Wang H;

XX WPI: 2000-514528/46.

XX P-PSDB: AAY95537.

XX Detergent composition comprising novel phenol oxidising enzyme obtained
XX from fungus or bacteria, useful for pulp and paper bleaching, bleaching
XX color of stains on fabric and for anti-dye redeposition

XX Disclosure; Fig 5A-B; 45pp; English.

CC The present sequence is that of the Stachybotrys chartarum MUC1 38898
CC cDNA encoding a phenol oxidising enzyme (see AAY95537). The invention
CC relates to detergent compositions comprising novel phenol oxidising
CC enzymes that are encoded by nucleic acids capable of hybridising to
CC the S. chartarum phenol oxidising enzyme gene (see AA50019), provided
CC the enzymes are capable of modifying the colour associated with dyes
CC or coloured compounds, and are produced from a bacterium, yeast or
CC fungus (see AAY9538-40). The phenol oxidising enzymes can be used
CC for pulp and paper bleaching, for bleaching the colour of stains on
CC fabric and for anti-dye transfer in detergent and textile
CC applications. They may also be capable of modifying the colour in
CC the absence or presence of an enhancer. Expression vectors and host
CC cells comprising a nucleic acid encoding a phenol oxidising enzyme,
CC methods for producing the phenol oxidising enzyme, and methods for
CC constructing expression hosts are provided.

XX Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;

Query Match

Best Local Similarity 36.1%; Score 27.4; DB 21; Length 1791;

Matches 43; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

OY 4 TTCATCAGACGCCGACATGCGCCACTTTGGCCGTGACGCGCGACTTCACTGCGAG 63
DB 577 TTCATCAGACGCTGAGATGCTTGTGTCAGCGCTGCGCTACATTATCAACGAC 636
OY 64 GTGCTCAAG 72

KM copper; metal cofactor; gene; plant; ds.
 XX
 OS Stachybotrys chartarum.
 XX
 PN WO200196543-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 14-JUN-2001; 2001WO-US19174.
 XX
 PR 15-JUN-2000; 2000US-211732P.
 XX
 PA (PROD-) PRODIGENE INC.
 XX (GENY) GENENCOR INC.
 PI Hood E, Howard JA, Bailey M, Van Gastel FJC, Ward M, Wang H;
 PI Woodard S;
 XX
 DR WPI; 2002-090204/12.
 XX
 PT Improving recovery of active enzyme e.g. laccase, which requires
 PT transitional metal cofactor e.g. copper for activity, from a plant, by
 PT introducing plant nucleotide sequences encoding the enzyme and exposing
 PT it to cofactor
 XX
 PS Example 5; Fig 16A-E; 81pp; English.
 XX
 CC The present invention describes a method for improving the recovery of
 CC an active enzyme from a plant where the enzyme requires a transitional
 CC metal cofactor for activity. The method comprises introducing into the
 CC plant nucleotide sequences encoding the enzyme and exposing the enzyme
 CC to the metal cofactor. The method is useful for improving recovery of
 CC active enzyme which requires a transitional metal cofactor for activity,
 CC preferably for improving recovery of active laccase which requires
 CC copper for activity. The method can be used for improving recovery of
 CC active organophosphate hydrolase (OPH, E.C. 3.1.8.1) which requires
 CC zinc, nickel, cobalt or manganese for activity, where the method further
 CC comprises adding bicarbonate ion salt. The present sequence encodes the
 CC fungal Stachybotrys chartarum laccase enzyme. Laccases are also called
 CC blue copper oxidases and use copper to accept and donate electrons in
 CC the oxidation and reduction of substrates.
 XX
 SQ Sequence 7248 BP; 1928 A; 1744 C; 1579 G; 1997 T; 0 other;

Query Match 36.1%; Score 27.4; DB 24; Length 7248;
 Best Local Similarity 62.3%; Pred. No. 26;
 Matches 43; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

OY 4 TTATCAAGACGGCGCATATGCGGCGTGACGACCGCATTCACCTGCGAG 63
 DB 5768 TTATCAAGACGCTGCTAGAAATGCTACTTGTGAGCTGGCGCATATATCAACGAC 5827
 OY 64 GTGGTCAAG 72
 DB 5828 GAGCTGAG 5836

Search completed: April 23, 2003, 15:42:04
 Job time : 2439.94 secs

DB 382 GluValValLysPro 386
 RESULT 2
 P00817
 methionine adenosyltransferase (EC 2.5.1.6) - rape (fragment)
 C:Species: Brassica napus (rape)
 C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 05-May-2000
 C:Accession: P00817
 R:Park, Y.S.; Kwak, J.M.; Kwon, O.Y.; Kim, Y.S.; Lee, D.S.; Cho, M.J.; Lee, H.H.; Nam, H.
 Plant Physiol. 103, 359-370, 1993
 A:Title: Generation of expressed sequence tags of random root cDNA clones of Brassica na
 A:Reference number: P00816; MUID:94302145; PMID:8029332
 A:Accession: P00817
 A:Molecule type: mRNA
 A:Residues: 1-68 <PAR>
 A:Experimental source: root, cv. Naeahan
 C:Superfamily: methionine adenosyltransferase
 C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
 Pred. No.: 1.31e-09 Length: 68
 Score: 120.00 Matches: 22
 Percent Similarity: 92.00% Conservative: 1
 Best Local Similarity: 88.00% Mismatches: 2
 Query Match: 86.96% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779B-1_COPY_160_235 (1-76) x P00817 (1-68)

QY 1 AGGTTATCAAGACCGCGCATACGGCCACTTGGCCGTACAGCCCGCCTTACCTGC 60
 DB 36 ArgPheLeuLysThrAlaIatYrGlyHisPheGlyArgAspAspProAspPheThrTrp 55

QY 61 GAGGTGTCACAGCC 75
 DB 56 GluValValLysPro 60

RESULT 3
 JN0131
 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana
 N:Alternate names: S-adenosylmethionine synthetase
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-May-2000
 C:Accession: JN0131
 R:Peleman, J.; Boerjan, W.; Engler, G.; Seurinck, J.; Bolterman, J.; Alliotte, T.; Van M
 Plant Cell 1, 81-93, 1989
 A:Title: Strong cellular preference in the expression of a housekeeping gene of Arabidop
 A:Reference number: JN0131; MUID:92386056; PMID:2535470
 A:Accession: JN0131
 A:Molecule type: DNA
 A:Residues: 1-393 <PEL>
 A:Cross-references: GB:M55077; NID:q166871; PIDN:AAA32868.1; PID:q166872
 A:Experimental source: var. K85
 A:Note: the sequence derived from var. Columbia differs from that shown in having 117-Gl
 A:Note: the authors translated the codon GAC for residue 117 as Glu
 C:Comment: S-Adenosylmethionine synthetase catalyzes the biosynthesis of adenosylmethio
 C:Genetics:
 A:Gene: sam-1
 C:Superfamily: methionine adenosyltransferase
 C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
 Pred. No.: 1.31e-09 Length: 393
 Score: 120.00 Matches: 22
 Percent Similarity: 92.00% Conservative: 1
 Best Local Similarity: 88.00% Mismatches: 2
 Query Match: 86.96% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779B-1_COPY_160_235 (1-76) x JN0131 (1-393)

QY 1 AGGTTATCAAGACCGCGCATACGGCCACTTGGCCGTACAGCCCGCCTTACCTGC 60

DB 361 ArgPheLeuLysThrAlaIatYrGlyHisPheGlyArgAspAspProAspPheThrTrp 380
 QY 61 GAGGTGTCACAGCC 75
 DB 381 GluValValLysPro 385

RESULT 4
 S38875
 methionine adenosyltransferase (EC 2.5.1.6) - tomato
 N:Alternate names: S-adenosyl-L-methionine synthetase
 C:Species: Lycopersicon esculentum (tomato)
 C:Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
 C:Accession: S46539; S38875
 R:Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.
 Plant Mol. Biol. 25, 217-227, 1994
 A:Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in
 A:Reference number: S46538; MUID:94289646; PMID:8018871
 A:Accession: S46539
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-393 <ES2>

Alignment Scores:
 Pred. No.: 1.31e-09 Length: 393
 Score: 120.00 Matches: 22
 Percent Similarity: 92.00% Conservative: 1
 Best Local Similarity: 88.00% Mismatches: 2
 Query Match: 86.96% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779B-1_COPY_160_235 (1-76) x S38875 (1-393)

QY 1 AGGTTATCAAGACCGCGCATACGGCCACTTGGCCGTACAGCCCGCCTTACCTGC 60
 DB 361 ArgPheLeuLysThrAlaIatYrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

QY 61 GAGGTGTCACAGCC 75
 DB 381 GluValValLysPro 385

RESULT 5
 S46538
 methionine adenosyltransferase (EC 2.5.1.6) - tomato
 N:Alternate names: S-adenosyl-L-methionine synthetase
 C:Species: Lycopersicon esculentum (tomato)
 C:Date: 26-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
 C:Accession: S46538; S38874
 R:Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.
 Plant Mol. Biol. 25, 217-227, 1994
 A:Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in
 A:Reference number: S46538; MUID:94289646; PMID:8018871
 A:Accession: S46538
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-393 <ESP>
 A:Cross-references: EMBL:Z24741; NID:q429103; PIDN:CAA80865.1; PID:q429104
 C:Superfamily: methionine adenosyltransferase
 C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
 Pred. No.: 1.31e-09 Length: 393
 Score: 120.00 Matches: 22
 Percent Similarity: 92.00% Conservative: 1
 Best Local Similarity: 88.00% Mismatches: 2
 Query Match: 86.96% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779B-1_COPY_160_235 (1-76) x S46538 (1-393)

Qy	1	AGGTTATCTCAAGACCGCCGATACGGCCACTTGGCCCGGAGACGACCGCCAGCTTTCACCTGCG	60
		:::	
Db	361	ArgpHeuEuyStrhAlaAaTyRgLyHtSpHeGlyArgAspAspProAspHeHtrTp	380
Qy	61	GAGTGGTCAAGCCC	75
Db	381	GluValValLysPro	385

RESULT 6

S:adenosylmethionine synthetase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C86155
R:Phenologist: A.; Ecker, J.R.; Palm, C.J.; Federici, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltli, R.; Marziani
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C86155
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-393 <STO>
A:Cross-references: GB:AE005172; NID:g9972389; PIDN:AAG10639.1; GSPDB:GM00141
C:Genetics:
A:Map position: 1
C:Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	1.31e-09	Length:	39
Score:	120.00	Matches:	22
Percent Similarity:	92.00%	Conservative:	1
Best Local Similarity:	88.00%	Mismatches:	2
Query Match:	86.96%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x C86155 (1-393)

Qy 1 AGGTTTCATCAAGACGCCCGCATACGGCCACTTTTGGCCGTGACGAGCGCGACTTCACCTTGC 60
|||||:::|||||
Db 361 ArgfhelEulwSThralaalaTyrgLYhISPhelcYArgspasproASpHeThTrp 380

QY	61	GAGGTGGTCAAGCCC	75
Db	381	GIuValVallyspro	385

RESULT 7

methionine adenosyltransferase (EC 2.5.1.6) - garden pea (fragment)
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C:Accession: T06592
R:Gomez, L.; Carriasco, P.
A:Submitted to the EMBL Data Library, January 1995
A:Description: Hormonal regulation of the S-adenosylmethionine synthase in pea ovaries
A:Reference number: Z15782
A:Accession: T06592
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-360 <GOM>
A:Cross-references: EMBL: L36680; NTD:g609556; PIDD:AAA58772.1; PID:g609557
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	5.23e-09	Length:	360
Score:	116.00	Matches:	21

Percent Similarity:	92.00%	Conservative:	2
Best Local Similarity:	84.00%	Mismatches:	2
Query Match:	84.06%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x T06592 (1-360)

```

QY      1 AGGTTTCATCAAGACCGCGGCATTACGGCCACTTTGGCGCGTACAGACCGCGGACTTTCACCTGCG 60
      |||:::|||||
Db    330 ArgPheLeuysThrIaIaIaTyrGlyHisPheGlyArgGluAspProAspPheThrTyr 34

```

Qy	61	GAGGTGGTCAAGCCC	75
Db	350	GluValValLysPro	354

RESULT 8
S66351
methionine adenosyltransferase

RESULT 8

methionine adenosyltransferase (EC 2.5.1.6) 1 - garden pea (fragment)
C:Species: *Pisum sativum* (garden pea)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-May-2000
C:Accession: S66351
R:Gomez-Gomez, L.; Carrasco, P.
Plant Mol. Biol. 30, 821-832, 1996
A:Title: Hormonal regulation of S-adenosylmethionine synthase transcripts in pea ovar
A:Reference number: S66351; MUID:96194463; PMID:8624412
A:Accession: S66351
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-56 <GOM>
A:Cross-references: EMBL:X82076; NID:6609222; PIDD:CAAS7580.1; PID:6609223
A:Note: the authors did not translate the codon for residue 1
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	5.22e-09	Length:	366
Score:	116.00	Matches:	21
Percent Similarity:	92.00%	Conservative:	2
Best Local Similarity:	84.00%	Mismatches:	2
Query Match:	84.06%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x S66351 (1-366)

Oy 1 AGGTCATCAAGACCGCCGCATAGGGCACTTTGGCCGTGACGACGCCGACTTTCACCTGC 60
|||||:::||||| ||||| ||||| ::||| |||||
Db 336 ArgPheLeuYstThraIaLaIaTyrGLynHSPheGlyArgGIuaSproAaspPheThrTrp 355

QY	61	GAGGTGGTCAAGCCC	75
Db	356	GIuValVallylsp	360

RESULT 9

probable s-radenosylmethionine synthetase, imported) - Arabidopsis thaliana
 C.Species: Arabidopsis thaliana (mouse-ear cress)
 C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C.Accession: G84785
 R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
 M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999
 A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A.Reference number: A84420; MUID:20083487; PMID:10617197
 A.Accession: G84785
 A.Status: Preliminary
 A.Molecule type: DNA
 A.Residues: 1-390 <SPD>
 A.Cross-references: GB:AE002093; NID:g4883604; PIDN:AMD31573.1; GSPDB:GN00139
 C.Genetics:
 A.Gene: At2g36680
 A.Map position: 2
 C.Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.: 7.38e-09 Length: 390
Score: 115.00 Matches: 22
Percent Similarity: 88.00% Conservative: 0
Best Local Similarity: 88.00% Mismatches: 3
Query Match: 83.33% Indels: 0
DB: 2 Gaps: 0

US-09-198-779b-1_COPY_160_235 (1-76) x G84785 (1-390)

OY 1 AGGTTATCAAGACCCCGCATACGCCACTTGGCCGAGACAGCCGACCTTCACTTC 60
Db 361 ArgPheGlnLysThrAlaIatyrGlnSphGlyArgAspAspProAspPheThrTrp 380
OY 61 GAGGTGTCACGCC 75
Db 381 GluValValLysPro 385

RESULT 10

J00410

methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana

N:Alternate names: S-adenosylmethionine synthetase

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-May-2000

C:Accession: J00410

R:Peleman, J.; Salto, K.; Cottyn, B.; Engler, G.; Seurinck, J.; Van Montagu, M.; Inze, D

Gene 84, 359-369, 1989

A:Title: Structure and expression analyses of the S-adenosylmethionine synthetase gene

A:Reference number: J00410; MUID:90128280; PMID:2482229

A:Accession: J00410

A:Molecule type: DNA

A:Residues: 1-393 <PEL>

A:Cross-references: GB:M3217; NID:9166873; PIDN:AAA32869.1; PID:9166874

C:Genetics:

A:Gene: sam-2

C:Superfamily: methionine adenosyltransferase

C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.: 7.38e-09 Length: 393
Score: 115.00 Matches: 22
Percent Similarity: 88.00% Conservative: 0
Best Local Similarity: 88.00% Mismatches: 3
Query Match: 83.33% Indels: 0
DB: 2 Gaps: 0

US-09-198-779b-1_COPY_160_235 (1-76) x J00410 (1-393)

OY 1 AGGTCATCAAGACCCCGCATACGCCACTTGGCCGAGACAGCCGACCTTCACTTC 60
Db 361 ArgPheGlnLysThrAlaIatyrGlnSphGlyArgAspAspProAspPheThrTrp 380
OY 61 GAGGTGTCACGCC 75
Db 381 GluValValLysPro 385

RESULT 11

S66352

methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea

C:Species: Pisum sativum (garden pea)

C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-May-2000

C:Accession: S66352; S52218

R:Gomez-Gomez, L.; Carrasco, P.

Plant Mol. Biol. 30, 821-832, 1996

A:Title: Hormonal regulation of S-adenosylmethionine synthase transcripts in pea ovaries

A:Reference number: S66351; MUID:96194463; PMID:862412

A:Accession: S66352

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-397 <GOM>

A:Cross-references: EMBL:X82077

R:Gomez, L.; Carrasco, P.

submitted to the EMBL Data Library, October 1994

A:Description: Hormonal regulation of the S-adenosylmethionine synthase in pea ovaries

A:Reference number: S52218

A:Accession: S52218

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-394, 'FPDSCITWFW' <GOM>

A:Cross-references: EMBL:X82077; NID:9609224; PIDN:CAA57581.1; PID:9609225

C:Superfamily: methionine adenosyltransferase

C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.: 7e-08 Length: 397
Score: 108.50 Matches: 22
Percent Similarity: 88.46% Conservative: 1
Best Local Similarity: 84.62% Mismatches: 2
Query Match: 78.62% Indels: 1
DB: 2 Gaps: 1

US-09-198-779b-1_COPY_160_235 (1-76) x S66352 (1-397)

OY 1 AGGTTCAAGACCCCGCATACGCCACTTGGCCGAGACAGCCGACCTTCACTTC 57
Db 363 ArgPheLeuLysThrAlaIatyrGlnSphGlySerAspAspAlaAspPheThr 382
OY 58 TGCAGGTGTCACGCC 75
Db 383 TrpGluValValLysPro 388

RESULT 12

T07899

methionine adenosyltransferase (EC 2.5.1.6) - Chlamydomonas reinhardtii (fragment)

N:Alternate names: S-adenosylmethionine synthetase

C:Species: Chlamydomonas reinhardtii

C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 05-May-2000

C:Accession: T07899

R:Kim, J.Y.; Lee, K.O.; Lee, S.H.

submitted to the EMBL Data Library, June 1997

A:Description: Chlamydomonas reinhardtii mRNA for S-adenosylmethionine synthetase.

A:Accession: T07899

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-179 <KIM>

A:Cross-references: EMBL:AF008568; NID:92454483; PIDN:AAE71833.1; PID:92454484

A:Experimental source: strain 137C

C:Genetics:

A:Gene: SAMS

C:Function:

A:Description: catalyzes the formation of S-adenosyl methionine with phosphate and py

C:Superfamily: methionine adenosyltransferase

C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.: 9.4e-07 Length: 179
Score: 101.00 Matches: 19
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 79.17% Mismatches: 4
Query Match: 73.19% Indels: 0
DB: 2 Gaps: 0

US-09-198-779b-1_COPY_160_235 (1-76) x T07899 (1-179)

OY 1 AGGTTCAAGACCCCGCATACGCCACTTGGCCGAGACAGCCGACCTTCACTTC 60
Db 153 ArgPheGlnLysThrAlaIatyrGlnSphGlySerAspAspAlaAspPheThrTrp 172
OY 61 GAGGTGTCACGCC 72
Db 173 GluThrValLys 176

RESULT 13

S49491

methionine adenosyltransferase (EC 2.5.1.6) - garden petunia

C:Species: Petunia x hybrida (garden petunia)

C>Date: 01-Feb-1995 #sequence_revision 10-Nov-1995 #text_change 05-May-2000

C:Accession: S49491

R:Iznaki, A.; Shoseyov, O.; Weiss, D.

submitted to the EMBL Data Library, October 1994

A:Description: Petunia cDNA encoding S-Adenosylmethionine synthetase.

A:Reference number: S49491

A:Accession: S49491

A:Molecule type: mRNA

A:Residues: 1-390 <12H>

A:Cross-references: EMBL:X82214; NID:9559505; PIDN:CAA57696.1; PID:9559506

C:Superfamily: methionine adenosyltransferase

C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	9.39e-07	Length:	390
Score:	101.00	Matches:	19
Percent Similarity:	83.33%	Conservative:	1
Best Local Similarity:	79.17%	Mismatches:	4
Query Match:	73.19%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779b-1_COPY_160_235 (1-76) x S49491 (1-390)

OY 1 AGGTCATCAAGACCGCCGACATTCGCGCGCGGACGCGCCGACTTCACCTGC 60

||||: ||||||||| ||||||||| ||||||||| ||||||||| |||||||||

Db 361 ArgTyrGlnLysThrAlaIaIaTyrcIyHisPheGlyArgAspAspProAspPheThrTrp 380

OY 61 GAGGTGTCACAG 72

||| |||||

Db 381 GluThrValLys 384

RESULT 14

S46540

methionine adenosyltransferase (EC 2.5.1.6) - tomato

N:Alternate names: S-adenosyl-L-methionine synthetase

C:Species: Lycopersicon esculentum (tomato)

C>Date: 26-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000

C:Accession: S46540; S38876

R:Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.

Plant Mol. Biol. 25, 217-227, 1994

A:Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in res

A:Reference number: S46538; MUID:94289646; PMID:8018871

A:Accession: S46540

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-390 <ESP>

A:Cross-references: EMBL:Z24743; NID:9429107; PIDN:CAA80867.1; PID:9429108

C:Superfamily: methionine adenosyltransferase

C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	9.39e-07	Length:	390
Score:	101.00	Matches:	19
Percent Similarity:	83.33%	Conservative:	1
Best Local Similarity:	79.17%	Mismatches:	4
Query Match:	73.19%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779b-1_COPY_160_235 (1-76) x S46540 (1-390)

OY 1 AGGTCATCAAGACCGCCGACATTCGCGCGGACGCGCCGACTTCACCTGC 60

||||: ||||||||| ||||||||| ||||||||| ||||||||| |||||||||

Db 361 ArgTyrGlnLysThrAlaIaIaTyrcIyHisPheGlyArgAspAspProAspPheThrTrp 380

OY 61 GAGGTGTCACAG 72

||| |||||

Db 381 GluThrValLys 384

RESULT 15

T10710

methionine adenosyltransferase (EC 2.5.1.6) - clove pink

N:Alternate names: S-adenosylmethionine synthetase

C:Species: Dianthus caryophyllus (clove pink)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-May-2000

C:Accession: T10710

R:Larsen, P.B.; Woodson, W.R.

submitted to the EMBL Data Library, April 1991

A:Description: Cloning and nucleotide sequence of a S-adenosylmethionine synthetase c

A:Reference number: 217091

A:Accession: T10710

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-396 <LAR>

A:Cross-references: EMBL:M61882; NID:9167961; PID:9304637

C:Gene: SAM2

C:Genetics:

C:Function:

A:Description: catalyzes the formation of S-adenosyl methionine with phosphate and py

C:Superfamily: methionine adenosyltransferase

C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	2.65e-06	Length:	396
Score:	98.00	Matches:	17
Percent Similarity:	83.33%	Conservative:	3
Best Local Similarity:	70.83%	Mismatches:	4
Query Match:	71.01%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779b-1_COPY_160_235 (1-76) x T10710 (1-396)

OY 1 AGGTCATCAAGACCGCCGACATTCGCGCGGACGCGCCGACTTCACCTGC 60

||||: ||||||||| ||||||||| ||||||||| ||||||||| |||||||||

Db 364 ArgTyrLeuLysThrAlaIaIaTyrcIyHisPheGlyArgAspAspProAspPheThrTrp 383

OY 61 GAGGTGTCACAG 72

||| |||||

Db 384 GluAlaIaLys 387

RESULT 16

G72228

S-adenosylmethionine synthetase - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: G72228

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: G72228

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <ARN>

A:Cross-references: GB:AE001807; GB:AE000512; NID:94982216; PIDN:AD36725.1; PID:9498

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM1658

C:Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	0.0107	Length:	395
Score:	74.00	Matches:	13
Percent Similarity:	88.89%	Conservative:	3
Best Local Similarity:	72.22%	Mismatches:	2
Query Match:	53.62%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779b-1_COPY_160_235 (1-76) x G72228 (1-395)

OY 10 AAGACCGCCGACATTCGCGCGGACGCGCCGACTTCACCTGCAG 63

||||: ||||||||| ||||||||| ||||||||| ||||||||| |||||||||

Db 364 LysThrAlaIaIaTyrcIyHisPheGlyArgAsnGluGluPheThrTrpGlu 381

Db 356 TVR Ser Lys Ser Ala Ala TVRG] VHis PheG] VArg] uG] uProG] uPhe Thr TrG] u 375

score:	83.00	malclines:	12
percent similarity:	72.22%	conservative:	1

```

Best Local Similarity: 66.67%      Mismatches: 5
Query Match: 47.10%               Indels: 0
DB: 2                             Gaps: 0

US-09-198-779B-1_COPY_160_235 (1-76) x D65657 (1-400)

QY 10 AAGACCGCGGATACGGCCACTTTGGCGGTGACGACGGCGACTTCACCTGCAG 63
DB 368 GlnThrAlaIatArgIyGlyHisPheGlyArgHisAspValaPleuProtrpIu 385

RESULT 21
A:adenosylmethionine synthetase U0412 [Imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: A82895
R:Glass, J.I.; Letkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to Genbank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir
A:Reference number: A82870
A:Accession: A82895
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <GLA>
A:Cross-references: GB:AE002138; GB:AF222894; NID:96899390; PIDN:AAF30823.1; GSPDB:GN001
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: mek; U0412
A:Genetic code: SGC3
C:Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.: 0.342      Length: 376
Score: 64.00          Matches: 10
Percent Similarity: 71.43%      Conservative: 5
Best Local Similarity: 47.62%      Mismatches: 6
Query Match: 46.38%      Indels: 0
DB: 2                Gaps: 0

US-09-198-779B-1_COPY_160_235 (1-76) x A82895 (1-376)

QY 1 AGGTCATCAGACCGCGCATACGGCCACTTTGGCGGTGACGACGGCGACTTCACCTGC 60
DB 343 LysTyrLeuProValaIatThrTyrGlyHisPheGlyArgAspAspLeuAsnLeuSerTrp 362

QY 61 GAG 63
DB 363 Glu 363

RESULT 22
S27257
methionine adenosyltransferase (EC 2.5.1.6) 2 alpha chain - human
N:Alternate names: renal methionine adenosyltransferase (MAT); S-adenosylmethionine synt
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
C:Accession: S27257
R:Horikawa, S.; Tsukada, K.
FEBS Lett. 312, 37-41, 1992
A:Title: Molecular cloning and developmental expression of a human kidney S-adenosylmeth
A:Reference number: S27257; MUID:93050159; PMID:1426236
A:Accession: S27257
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-395 <HOR>
A:Cross-references: EMBL:X68836; GB:SA47859; NID:936326; PIDN:CAA48726.1; PID:936327
C:Genetics:
A:Gene: GDB:MAT2A; SAMS2; MAT2A
A:Cross-references: GDB:136213; OMIM:601468
A:Map position: 2p11.2-2p11.2
A:Introns: 15/2; 256/3
C:Complex: heterodimer of catalytic alpha and regulatory beta chains
C:Function:
A:Description: catalyzes the formation of S-adenosyl methionine with phosphate and pyrop

```

```

A:Pathway: one-carbon metabolism
C:Superfamily: methionine adenosyltransferase
C:Keywords: ATP; heterodimer; kidney; magnesium; metalloprotein; one-carbon metabolism
F:276-286/Region: nucleotide-binding motif A (P-loop) #status atypical
F:31/Binding site: magnesium 2 (Asp) #status predicted
F:285,289/Active site: Lys #status predicted
F:291/Binding site: magnesium 1 (Asp) #status predicted

Alignment Scores:
Pred. No.: 0.483      Length: 395
Score: 63.00          Matches: 14
Percent Similarity: 71.43%      Conservative: 1
Best Local Similarity: 66.67%      Mismatches: 4
Query Match: 45.65%      Indels: 2
DB: 1                Gaps: 1

US-09-198-779B-1_COPY_160_235 (1-76) x S27257 (1-395)

QY 10 AAGACCGCGGATACGGCCACTTTGGCGGTGACGACGGCGACTTCACCTGCAGGTGTC 69
DB 373 ArgThrAlaIatArgIyGlyHisPheGlyArgAsp-----SerPheProtrpIuValaPro 390

QY 70 ANG 72
DB 391 Lys 391

RESULT 23
A37118
methionine adenosyltransferase (EC 2.5.1.6) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 05-May-2000
C:Accession: A37118
R:Horikawa, S.; Sasuga, J.; Shimizu, K.; Ozasa, H.; Tsukada, K.
J. Biol. Chem. 265, 13683-13686, 1990
A:Title: Molecular cloning and nucleotide sequence of cDNA encoding the rat kidney S-
A:Reference number: A37118; MUID:90337979; PMID:1696256
A:Accession: A37118
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-395 <HOR>
A:Cross-references: GB:J05571; NID:9206845; PIDN:AAA42106.1; PID:9206846
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.: 0.483      Length: 395
Score: 63.00          Matches: 14
Percent Similarity: 71.43%      Conservative: 1
Best Local Similarity: 66.67%      Mismatches: 4
Query Match: 45.65%      Indels: 2
DB: 2                Gaps: 1

US-09-198-779B-1_COPY_160_235 (1-76) x A37118 (1-395)

QY 10 AAGACCGCGGATACGGCCACTTTGGCGGTGACGACGGCGACTTCACCTGCAGGTGTC 69
DB 373 ArgThrAlaIatArgIyGlyHisPheGlyArgAsp-----SerPheProtrpIuValaPro 390

QY 70 ANG 72
DB 391 Lys 391

RESULT 24
H86976
probable S-adenosylmethionine synthase [Imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: H86976
R:Coile, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R.; Davies, R.M.; Devlin, K.; Duthey, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holro
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;

```

A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MID:21128732; PMID:11234002
A:Accession: H86976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-403 <STO>
A:Cross-references: GB:AL450380; NID:g13092748; PIDN:CAC30052.1; GSPDB:GNO0147
C:Genetics:
A:Gene: metK
C:Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.: 0.483 Length: 403
Score: 63.00 Matches: 11
Percent Similarity: 70.00% Conservative: 3
Best Local Similarity: 55.00% Mismatches: 6
Query Match: 45.65% Indels: 0
Gaps: 0
DB: 2

US-09-198-779b-1_copy_160_235 (1-76) x H86976 (1-403)

OY 4 TTCATCAGACCGCCGATACGGCCACTTGGCCGTGACGCGCCGACTTCACCTGCGAG 63
Db 372 TTTAAlaInhrAlaAlaIatYrGlnHisrPhcGlyArGrhAspValGluLeuProTprGlu 331

RESULT 25
F90599
hypothetical protein MYPV_7020 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: F90599
R:Chambaud, I.; Helling, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MID:21267165; PMID:11353084
A:Accession: F90599
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <RUR>
A:Cross-references: GB:AL445566; PID:g14090117; PIDN:CAC13875.1; GSPDB:GNO0153
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPV_7020
A:Genetic code: GCG3
C:Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.: 0.965 Length: 376
Score: 61.00 Matches: 10
Percent Similarity: 66.67% Conservative: 4
Best Local Similarity: 47.62% Mismatches: 7
Query Match: 44.20% Indels: 0
Gaps: 0
DB: 2

US-09-198-779b-1_copy_160_235 (1-76) x F90599 (1-376)

OY 1 AGCTTATCATGACCGCCGATACGGCCACTTGGCCGTGACGCGCCGACTTCACCTGCG 60
Db 343 LysTlYrPherGrhTsrPhrPhcGlnHisrPhcGlyArGrhAspValGluLeuProTprGlu 362

OY 61 GAG 63
Db 363 Glu 363

RESULT 26
D71964
S-adenosylmethionine synthetase - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 18-Jun-1999
C:Accession: D71964
R:Alm, R.A.; Liang, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doly, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Werberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p
A:Reference number: A71800; MID:99120557; PMID:9923682
A:Accession: D71964
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-385 <ARN>
A:Cross-references: GB:AE001456; GB:AE001439; NID:g4154689; PIDN:AA05755.1; PID:g415
A:Experimental source: strain J99
C:Genetics:
A:Gene: metK
C:Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.: 0.965 Length: 385
Score: 61.00 Matches: 11
Percent Similarity: 82.35% Conservative: 3
Best Local Similarity: 64.71% Mismatches: 3
Query Match: 44.20% Indels: 0
Gaps: 0
DB: 2

US-09-198-779b-1_copy_160_235 (1-76) x D71964 (1-385)

OY 13 ACCGCGCATACGGCCACTTGGCCGTGACGCGCCGACTTCACCTGCGAG 63
Db 355 ThrSerAlaTyrGlnHisrPhcGlyArGrhAspValGluLeuGluPhrThrTprGlu 371

RESULT 27
E64544
methionine adenosyltransferase (EC 2.5.1.6) 2 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 05-May-2000
C:Accession: E64544
R:Tomp, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey,
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MID:97394467; PMID:9252185
A:Accession: E64544
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-385 <TON>
A:Cross-references: GB:AE000540; GB:AE000511; NID:g2313287; PIDN:AA07267.1; PID:g231
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.: 0.965 Length: 385
Score: 61.00 Matches: 11
Percent Similarity: 82.35% Conservative: 3
Best Local Similarity: 64.71% Mismatches: 3
Query Match: 44.20% Indels: 0
Gaps: 0
DB: 2

US-09-198-779b-1_copy_160_235 (1-76) x E64544 (1-385)

OY 13 ACCGCGCATACGGCCACTTGGCCGTGACGCGCCGACTTCACCTGCGAG 63
Db 355 ThrSerAlaTyrGlnHisrPhcGlyArGrhAspValGluLeuGluPhrThrTprGlu 371

RESULT 28
F89964
S-adenosylmethionine synthetase [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: F89964
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratastu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89964
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-398 <KIR>
A:Cross-references: GB:BA000018; PID:913701583; PIDN:BA842876.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: metK
C:Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.: 0.965 Length: 398
Score: 61.00 Matches: 12
Percent Similarity: 72.22% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 5
Query Match: 44.20% Indels: 0
DB: 2 Gaps: 0

US-09-198-779b-1_COPY_160_235 (1-76) x F89964 (1-398)

OY 10 AAGACCGCGCATACGGCCACTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
Db 367 GlnThrAlaAlaIaTyrGlyHisPheGlyArgThrAspValaGluLeuProTprGlu 384

RESULT 29
D84062
S:adenosylmethionine synthetase metK [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: D84062
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: D84062
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-399 <STO>
A:Cross-references: GB:AP001518; GB:BA000004; NID:910175792; PIDN:BA807019.1; GSPDB:GN00
C:Genetics:
A:Experimental source: strain C-125
C:Genetics:
A:Gene: metK
C:Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.: 0.965 Length: 399
Score: 61.00 Matches: 11
Percent Similarity: 72.22% Conservative: 2
Best Local Similarity: 61.11% Mismatches: 5
Query Match: 44.20% Indels: 0
DB: 2 Gaps: 0

US-09-198-779b-1_COPY_160_235 (1-76) x D84062 (1-399)

OY 10 AAGACCGCGCATACGGCCACTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
Db 370 GlnThrAlaAlaIaTyrGlyHisPheGlyArgThrAspValaGluLeuProTprGlu 387

RESULT 30
F86862
methionine adenosyltransferase (EC 2.5.1.6) [imported] - Lactococcus lactis subsp. lacti
N:Alternate names: S-adenosylmethionine synthetase
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: F86862
R:Boitlin, A.; Winkler, P.; Mauger, S.; Jallion, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: F86862
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-399 <STO>
A:Cross-references: GB:AE005176; PID:912724937; PIDN:AAK06000.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: metK
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.: 0.965 Length: 399
Score: 61.00 Matches: 11
Percent Similarity: 72.22% Conservative: 2
Best Local Similarity: 61.11% Mismatches: 5
Query Match: 44.20% Indels: 0
DB: 2 Gaps: 0

US-09-198-779b-1_COPY_160_235 (1-76) x F86862 (1-399)

OY 10 AAGACCGCGCATACGGCCACTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
Db 368 GlnThrAlaAlaIaTyrGlyHisPheGlyArgThrAspValaGluLeuProTprGlu 385

RESULT 31
AD1654
S-methionine adenosyltransferase homolog metK [imported] - Listeria innocua (strain C
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AD1654
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fsihl,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maltouram, A.;
Ok, C.; Schueter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1654
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-399 <GLA>
A:Cross-references: GB:A1592022; PIDN:CACG7004.1; PID:916414260; GSPDB:GN00178
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: metK
C:Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.: 0.965 Length: 399
Score: 61.00 Matches: 11
Percent Similarity: 72.22% Conservative: 2
Best Local Similarity: 61.11% Mismatches: 5
Query Match: 44.20% Indels: 0
DB: 2 Gaps: 0

US-09-198-779b-1_COPY_160_235 (1-76) x AD1654 (1-399)

OY 10 AAGACCGCGCATACGGCCACTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
Db 368 GlnThrAlaAlaIaTyrGlyHisPheGlyArgThrAspValaGluLeuProTprGlu 385

RESULT 32
AH1282
S-methionine adenosyltransferase homolog metK [imported] - Listeria monocytogenes (st
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AH1282
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fsihl,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maltouram, A.;
Ok, C.; Schueter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679666
A:Accession: AH1282
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-399 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC99742.1; PID:916411100; GSPDB:GN00177
A:Experimental source: strain ESD-e
C:Genetics:
A:Gene: metK
C:Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.: 0.965 Length: 399
Score: 61.00 Matches: 11
Percent Similarity: 72.22% Conservative: 2
Best Local Similarity: 61.11% Mismatches: 5
Query Match: 44.20% Indels: 0
DB: 2 Gaps: 0

US-09-198-779B-1_COPY_160_235 (1-76) x AH1282 (1-399)

OY 10 AAGACCCGCGATACGCGCACTTGGCGTGAAGCGCGACTTCACCTGCGAG 63
::: |||||::: ||||| ||| |||
DB 368 GlnThrAlaIalaphcglYhispheglYargserAspLeuAspLeuProtrpglu 385

RESULT 33
F70899
Probable metK protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: F70899
R:Colb, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Genies, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: F70899
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-403 <COL>
A:Cross-references: GB:Z80108; GB:AL123456; NID:93256012; PIDN:CAN02194.1; PID:93256013
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: metK
C:Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.: 0.965 Length: 403
Score: 61.00 Matches: 11
Percent Similarity: 65.00% Conservative: 2
Best Local Similarity: 55.00% Mismatches: 7
Query Match: 44.20% Indels: 0
DB: 2 Gaps: 0

US-09-198-779B-1_COPY_160_235 (1-76) x F70899 (1-403)

OY 4 TTCATCAAGACCGCGCGCATACGCGCACTTGGCGTGAAGCGACTTCACCTGCGAG 63
::: |||||::: ||||| ||| |||
DB 372 TyrAlaProThrAlaIalaphcglYhispheglYargThrAspValcIuLeuProtrpglu 391

RESULT 34
B97403
methionine adenosyltransferase (EC 2.5.1.6) - Agrobacterium tumefaciens (strain C58, Cent
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: B97403
R:Goodner, B.; Hinkle, G.; Gelling, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; PMID:11743194

A:Accession: B97403
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-420 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK86179.1; PID:915155274; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_632
A:Map position: circular chromosome
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.: 0.965 Length: 420
Score: 61.00 Matches: 14
Percent Similarity: 63.33% Conservative: 5
Best Local Similarity: 46.67% Mismatches: 5
Query Match: 44.20% Indels: 6
DB: 2 Gaps: 2

US-09-198-779B-1_COPY_160_235 (1-76) x B97403 (1-420)

OY 4 TTCATCAAGACCGCGCGCATACGCGCACTTGGCGTGAAC-----GACGCGGACTTC 54
::: |||||::: ||||| ||| |||
DB 384 TyrAlaIalaphcglYhispheglYargserAspLeuAspLeuProtrpglu 403

OY 55 ACCTGCGAG-----GTGTCAGAGCC 75
::: |||
DB 404 SerTrpGluYsLeuAspLeuValYsPro 413

RESULT 35
AB2621
S-adenosylmethionine synthetase metK [imported] - Agrobacterium tumefaciens (strain C
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C:Accession: AB2621
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, M.; Grant, C.; Guenther, D.; Kutayvin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AB2621
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-420 <KUR>
A:Cross-references: GB:AE008688; PIDN:AL41384.1; PID:917738701; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: metK
A:Map position: circular chromosome
C:Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.: 0.965 Length: 420
Score: 61.00 Matches: 14
Percent Similarity: 63.33% Conservative: 5
Best Local Similarity: 46.67% Mismatches: 5
Query Match: 44.20% Indels: 6
DB: 2 Gaps: 2

US-09-198-779B-1_COPY_160_235 (1-76) x AB2621 (1-420)

OY 4 TTCATCAAGACCGCGCGCATACGCGCACTTGGCGTGAAC-----GACGCGGACTTC 54
::: |||||::: ||||| ||| |||
DB 384 TyrAlaIalaphcglYhispheglYargserAspLeuAspLeuProtrpglu 403

OY 55 ACCTGCGAG-----GTGTCAGAGCC 75
::: |||
DB 404 SerTrpGluYsLeuAspLeuValYsPro 413

RESULT 36

S74736
 methionine adenosyltransferase (EC 2.5.1.6) - *Synechocystis* sp. (strain PCC 6803)
 N:Alternate names: protein sll0927; S-adenosylmethionine synthetase
 C:Species: *Synechocystis* sp.
 A:Valley: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
 C:Accession: S74736
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Matsubae, A.; Yamada, M.; Yasuda
 DNA Res. 3: 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
 S.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S74736
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-409 <KAN>
 A:Cross-references: EMBL:D90901; GB:AE001339; MID:91651897; PIDN:BAAL6887.1; PID:9165196
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Gene: metX
 A:Start codon: GTG
 C:Superfamily: methionine adenosyltransferase
 C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
 Pred. No.: 1.15 Length: 409
 Score: 60.50 Matches: 13
 Percent Similarity: 68.18% Conservative: 2
 Best Local Similarity: 59.09% Mismatches: 6
 Query Match: 43.84% Indels: 1
 Gaps: 2

US-09-198-779b-1_COPY_160_235 (1-76) x S74736 (1-409)

OY 1 AGGTCATCAG--ACCGCCGATACGGCCACTTGGCCGTGACGACCCGACTTACAC 57
 Db 367 ArgPheTyrGlnAspValAlaIatTgIyHisPheGlyArgAsnAspLeuAspLeuPro 386

OY 58 TGGCAG 63
 Db 387 TrpGlu 388

RESULT 37
 E82319
 S-adenosylmethionine synthase WC0472 [imported] - *Vibrio cholerae* (strain N16961 serogroup
 C:Species: *Vibrio cholerae*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: E82319
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
 charlson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
 L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406: 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: E82319
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-385 <HEI>
 A:Cross-references: GB:AE004133; GB:AE003852; MID:96654889; PIDN:AAE93645.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC0472
 A:Map position: 1
 C:Superfamily: methionine adenosyltransferase

Alignment Scores:
 Pred. No.: 1.36 Length: 385
 Score: 60.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 83.33% Mismatches: 0
 Query Match: 43.48% Indels: 0
 Gaps: 2

US-09-198-779b-1_COPY_160_235 (1-76) x E82319 (1-385)

OY 10 AAGACCGCCGATACGGCCACTTGGCCGTGACGAC 45
 Db 355 LysThrAlaIatTgIyHisPheGlyArgGluGlu 366

RESULT 38
 A71281
 Probable S-adenosylmethionine synthetase (metK) - *Syphilis spirochete*
 C:Species: *Treponema pallidum* subsp. *pallidum* (*Syphilis spirochete*)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 18-Jun-1999
 C:Accession: A71281
 R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G.
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uitterback, T.; M
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281: 375-388, 1998
 A:Title: Complete genome sequence of *Treponema pallidum*, the *Syphilis spirochete*.
 A:Reference number: A71250; MUID:98332770; PMID:9665876
 A:Accession: A71281
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-396 <COL>
 A:Cross-references: GB:AE001250; GB:AE000520; MID:93323096; PIDN:AAE65758.1; PID:9332
 A:Experimental source: strain Nichols
 C:Genetics:
 A:Gene: TP0794
 C:Superfamily: methionine adenosyltransferase

Alignment Scores:
 Pred. No.: 1.93 Length: 396
 Score: 59.00 Matches: 13
 Percent Similarity: 54.55% Conservative: 5
 Best Local Similarity: 39.39% Mismatches: 7
 Query Match: 42.75% Indels: 8
 Gaps: 2

US-09-198-779b-1_COPY_160_235 (1-76) x A71281 (1-396)

OY 1 AGGTCATCAGACCGCCGATACGGCCACTTGGCCGTGACGAC----- 45.
 Db 355 ArgTyrArgSerThrAlaValTgIyHisPheGlyArgGluGlnPheProTrpGluArg 374

OY 46 GCCGACTTCACCTGCGAGGTG-----GTCAAGCC 75
 Db 375 ThrAspValCysAspLeuGlnArgAlaValArgPro 387

RESULT 39
 A47151
 methionine adenosyltransferase (EC 2.5.1.6) - mouse
 N:Alternate names: S-adenosylmethionine synthetase
 C:Species: *Mus musculus* (house mouse)
 C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-May-2000
 C:Accession: A47151
 R:Sakata, S.F.; Shelly, L.L.; Ruppert, S.; Schutz, G.; Chou, J.Y.
 J. Biol. Chem. 268: 13978-13986, 1993
 A:Title: Cloning and expression of murine S-adenosylmethionine synthetase.
 A:Reference number: A47151; MUID:93300783; PMID:8314764
 A:Accession: A47151
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-396 <SAK>
 A:Experimental source: liver
 A:Note: sequence inconsistent with the nucleotide translation;
 C:Superfamily: methionine adenosyltransferase
 C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
 Pred. No.: 1.93 Length: 396
 Score: 59.00 Matches: 13
 Percent Similarity: 71.43% Conservative: 2
 Best Local Similarity: 61.90% Mismatches: 4

Query Match:	42.75%	Indels:	2
DB:	2	Gaps:	1
US-09-198-779B-1_COPY_160_235 (1-76) x A47151 (1-396)			
OY	10	AAGACCGCCGACATAGCGCCACTTTGGCCGTGACGACGCCGACTTCACCTCGAGGTGTC	69
DB	374	LysHrAlaCysTyrGlyHisPheGlyArg-----SerGluPheProTyrGluValPro	391
OY	70	AAG 72	
DB	393	Lys 393	
RESULT 40			
S06114			
methionine adenosyltransferase (EC 2.5.1.6) - rat			
N:Alternate names: S-adenosylmethionine synthetase			
C:Species: Rattus norvegicus (Norway rat)			
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 05-May-2000			
C:Accession: S06114; S18256; S18257			
R:Horikawa, S.; Ishikawa, M.; Ozasa, H.; Tsukada, K.			
Eur. J. Biochem. 184, 497-501, 1989			
A:Title: Isolation of a cDNA encoding the rat liver S-adenosylmethionine synthetase.			
A:Reference number: S06114; MUID:90032633; PMID:2806235			
A:Accession: S06114			
A:Molecule type: mRNA			
A:Residues: 1-397 <HOK>			
A:Cross-references: EMBL:X15734; NID:g57183; PIDN:CAA33754.1; PID:g57184			
R:Mato, J.M.			
submitted to the EMBL Data Library, July 1991			
A:Reference number: S18256			
A:Accession: S18256			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-397 <MAT>			
A:Cross-references: EMBL:X60822			
R:Alvarez, L.; Asuncion, M.; Corrales, F.; Pajares, M.A.; Mato, J.M.			
FEBS Lett. 290, 142-146, 1991			
A:Title: Analysis of the 5' non-coding region of rat liver S-adenosylmethionine synthetase			
A:Reference number: S18257; MUID:92008649; PMID:1915866			
A:Accession: S18257			
A:Status: translation not shown			
A:Molecule type: mRNA			
A:Residues: 1-46 <ALV>			
A:Cross-references: EMBL:X60822			
C:Superfamily: methionine adenosyltransferase			
C:Keywords: S-adenosylmethionine; transferase			
Alignment Scores:			
Pred. No.:	1.93	Length:	397
Score:	59.00	Matches:	13
Percent Similarity:	71.43%	Conservative:	4
Best Local Similarity:	61.90%	Mismatches:	2
Query Match:	42.75%	Indels:	2
	2	Gaps:	1
US-09-198-779B-1_COPY_160_235 (1-76) x S06114 (1-397)			
OY	10	AAGACCGCCGACATAGCGCCACTTTGGCCGTGACGACGCCGACTTCACCTCGAGGTGTC	69
DB	375	LysHrAlaCysTyrGlyHisPheGlyArg-----SerGluPheProTyrGluValPro	392
OY	70	AAG 72	
DB	393	Lys 393	
RESULT 41			
H70866			
hypothetical protein RV2473 - Mycobacterium tuberculosis (strain H37RV)			
C:Species: Mycobacterium tuberculosis			
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999			
C:Accession: H70866			
R:Cole, S.T.; Brosch, P.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.			

```

; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
; Rajandram, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
; Nature 393, 537-544, 1998
; Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
; A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
; A:Reference number: A70500; MUID:98295987; PMID:9634230
; A:Accession: H70866
; A:Status: preliminary; nucleic acid sequence not shown; translation not shown
; A:Molecule type: DNA
; A:Residues: 1*238 <COL>
; A:Cross-references: GB:AL021246; GB:AL123456; NID:93261507; PIDN:CAAI6050.1; PID:e1233
; A:Experimental source: Strain H37Rv
; C:Genetics:
; A:Gene: RV2473

Alignment Scores:
Pred. No.:          2 29          Length:          238
Score:              58.50         Matches:          13
Percent Similarity: 60.87%        Conservative:    1
Best Local Similarity: 56.52%      Mismatches:     4
Query Match:        42.39%         Indels:         5
DB:                  2            Gaps:              1

US-09-198-779B-1_COPY_160_235 (1-76) x H70866 (1-238)

OY      2  GGTTCATCAAGACCGCCGCATACGCCACTTTGGCCGTGACGACCGCAGCTTCACCTGCG 61
          |||||||
Db       66  GlycerSerArgProAlaProSer-----ThrThrProArgSerProGly 80
          |||||||

OY      62  AGGTGTGCA 70
          |||||||
Db       81  ArgTyrSer 83

RESULT 42
E84977
Methionine adenosyltransferase (EC 2.5.1.6) [Imported] - Buchnera sp. (strain APS)
N:Alternate names: S-adenosylmethionine synthetase
C:Species: Buchnera sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: E84977
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A:Reference number: AB4930; MUID:20445173; PMID:10993077
A:Accession: E84977
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-378 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
; A:Gene: metK; BU408
; C:Superfamily: methionine adenosyltransferase
; C:Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:          2 73          Length:          378
Score:              58.00         Matches:          9
Percent Similarity: 85.71%        Conservative:    3
Best Local Similarity: 64.29%      Mismatches:     2
Query Match:        42.03%         Indels:         0
DB:                  2            Gaps:              0

US-09-198-779B-1_COPY_160_235 (1-76) x E84977 (1-378)

OY      4  TTTCATCAAGACCGCCGCATACGCCACTTTGGCCGTGACGAC 45
          :::::|||||
Db       352  TyrlenuSThrAlaValTyrGlyIshpGhglYargTgscu 365
          :::::|||||

microtubule-associated protein - fruit fly (Drosophila melanogaster)
;Species: Drosophila melanogaster

```


C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
 C:Accession: T13845
 R:Saunders, R.D.; Avides, M.C.; Howard, T.; Gonzalez, C.; Glover, D.M.
 J. Cell Biol. 137, 881-890, 1997
 A:Title: The drosophila gene abnormal spindle encodes a microtubule-associated protein
 A:Reference number: 21792; MUID:97296495; PMID:9151690
 A:Accession: T13845
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1861 <SAU>
 A:Cross-references: EMBL:U95171; MID:91930121; PID:91930122; PIDN:AAB51540.1
 C:Genetics:
 A:Gene: asp
 A:Cross-references: Flybase:Fbgp000140
 C:Function:
 A:Description: is required for the normal function of the mitotic spindle

Alignment Scores:
 Pred. No.: 2.72 Length: 1861
 Score: 58.00 Matches: 10
 Percent Similarity: 58.33% Conservative: 4
 Best Local Similarity: 41.67% Mismatches: 10
 Query Match: 42.03% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779b-1_COPY_160_235 (1-76) x T13845 (1-1861)

OY 5 TCATCAGAGCGCGCATACGCGCCCTTGCGCCGAGCAGCGACTTCACCTGCGAGG 64
 Db 83 AAlaAlaAlaProPseRerLysGlnThrTrpArgValThrAlaProSerArgProAlaAla 102
 OY 65 TGGTCAGAGCCCC 76
 Db 103 TrpAlaHisPro 106

RESULT 44
 AE2211
 S-adenosylmethionine synthetase [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AE2211
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguen, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete genome sequence of the filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AE2211
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-394 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA074943.1; PID:917132339; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all3244
 C:Superfamily: methionine adenosyltransferase

Alignment Scores:
 Pred. No.: 3.85 Length: 394
 Score: 57.00 Matches: 11
 Percent Similarity: 60.00% Conservative: 1
 Best Local Similarity: 55.00% Mismatches: 8
 Query Match: 41.30% Indels: 0
 DB: 2 Gaps: 0

US-09-198-779b-1_COPY_160_235 (1-76) x AE2211 (1-394)

OY 10 AAGACCGCGCATACGCGCACTTGGCGCGTGAAGCGCGCACTTCACCTGCGAGGTGTC 69
 Db 369 LysLeuAlaAlaIatyrGlyHisValGlyArgGlnAspIleAspLeuProTyrGluLysIle 388

RESULT 45
 T50705

gamma-aminobutyrate aminotransferase (EC 2.6.1.-) rhaA homolog [imported] - Rhodobact
 N:Alternate names: pyridoxal-phosphate dependent aminotransferase
 C:Species: Rhodobacter sphaeroides
 C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
 C:Accession: T50705
 R:Choudhary, M.; Kaplan, S.
 Nucleic Acids Res. 28, 862-867, 2000
 A:Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides
 A:Reference number: 225222; MUID:20115911; PMID:10648776
 A:Accession: T50705
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-447 <CHO>
 A:Cross-references: EMBL:AF195122; PIDN:AAF24249.1
 A:Experimental source: strain 2.4.1
 C:Genetics:
 A:Gene: rhaA
 C:Keywords: aminotransferase

Alignment Scores:
 Pred. No.: 3.85 Length: 447
 Score: 57.00 Matches: 11
 Percent Similarity: 55.56% Conservative: 4
 Best Local Similarity: 40.74% Mismatches: 8
 Query Match: 41.30% Indels: 4
 DB: 2 Gaps: 1

US-09-198-779b-1_COPY_160_235 (1-76) x T50705 (1-447)

OY 8 TCATCAGAGCGCGC-----CATACGCGCCACTTGGCGCGTGAAGCGCGCACTTCA 55
 Db 5 SerLeuProProArgGlyAlaAlaHisGluProAlaMetProCysArgThrProserAla 24
 OY 56 CCTGCGAGGTGTCAGAGCCCC 76
 Db 25 ProAlaArgTyrThrCysPro 31

Search completed: April 23, 2003, 12:08:01
 Job time : 8.33333 secs

THIS PAGE BLANK (USPTO)

OM nucleic - nucleic search, using sw model

Run on: April 23, 2003, 12:06:52 ; Search time 89.0694 Seconds
(without alignments)

3059.318 Million cell updates/sec

Title: US-09-198-779B-1_COPY_1_121

Sequence: 1 gtttccgtctagctcgt.....cagyacacaacagctacgt 121

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 08

Listing first 50 summaries

Database : N_Geneseq_101002: *

1:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24:	/SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	121	100.0	2061	21	AAA48574	CDNA encoding corn
2	29.2	24.1	2604	21	AAA48576	CDNA encoding whea
3	28.8	23.8	705	24	ABQ25086	Oligonucleotide Id
c 4	28.8	23.8	705	24	ABQ25087	Oligonucleotide Id
5	28.8	23.8	1519	20	AAV64373	GABA-gated chlorid
6	28.6	23.6	405	23	ABV48454	Human prostate exp
7	28.2	23.3	297	16	AAO88698	Beta-amyloid precu
8	28.2	23.3	300	24	AAK99387	DNA of wild type C
9	28	23.1	1357	21	AAC79021	Human secreted pro

C	10	27.6	22.8	1086	23	ABL04430	Drosophila melanog
C	11	27.6	22.8	3205	23	ABL04431	Drosophila melanog
C	12	27.6	22.8	3457	23	ABL04426	Drosophila melanog
C	13	27.4	22.6	4659	23	ABL28895	Drosophila melanog
C	14	27.4	22.6	7643	23	ABL28894	Drosophila melanog
C	15	27.4	22.6	32042	20	AAZ09252	Drosophila melanog
C	16	27.4	22.6	32042	22	AAE30011	Human CARD-4 DNA.
C	17	27.4	22.6	32042	22	AAE30011	Human CARD-4 gene.
C	18	27	22.3	628	24	ABL40765	Genomic DNA of hum
C	19	27	22.3	628	24	ABQ25024	Oligonucleotide fo
C	20	26.8	22.1	374	23	ABQ25025	Oligonucleotide fo
C	21	26.8	22.1	408	22	ABV54453	Human prostate exp
C	22	26.8	22.1	486	21	AAI86054	Human polynucleoti
C	23	26.8	22.1	1004	21	AAZ97180	Human prostate can
C	24	26.8	22.1	2033	22	AAZ97180	Human prostate can
C	25	26.8	22.1	2037	21	AAZ99961	Zea mays modified
C	26	26.8	22.1	2650	22	AAH14585	Nucleotide sequenc
C	27	26.8	22.1	2897	22	AAH16327	Human cDNA sequenc
C	28	26.8	22.1	3095	17	AAAT31290	Human cDNA sequenc
C	29	26.8	22.1	13255	23	ABLI6634	Mouse poly-I immunog
C	30	26.8	22.1	29392	19	AAV15422	Drosophila melanog
C	31	26.8	22.1	33513	22	AAK78746	Mouse poly Ig rece
C	32	26.6	22.0	294	9	AAH81865	Human Immune/haem
C	33	26.6	22.0	297	16	AAO88696	Clone Aml encoding
C	34	26.6	22.0	297	16	AAO88697	Beta-amyloid precu
C	35	26.6	22.0	300	24	AAO42665	Beta-amyloid precu
C	36	26.6	22.0	300	24	AAK99386	Full-length beta-g
C	37	26.6	22.0	303	21	AAA39488	DNA of wild type C
C	38	26.6	22.0	309	16	AAO88698	Human APP C100 DN
C	39	26.6	22.0	309	16	AAO88699	Beta-amyloid precu
C	40	26.6	22.0	315	22	AAO88700	Beta-amyloid precu
C	41	26.6	22.0	315	22	AAAD20982	Human recombinant
C	42	26.6	22.0	337	24	AAAD23935	Gamma-secretase su
C	43	26.6	22.0	336	17	AAIT80882	Familial Alzheimer
C	44	26.6	22.0	337	14	AAO59415	Human brain Express
C	45	26.6	22.0	354	19	AAV07188	Flag-amyloid prote
C	46	26.6	22.0	354	19	AAV20379	DNA for App C-term
C	47	26.6	22.0	354	21	AAA39490	Human APP signal P
C	48	26.6	22.0	354	22	AAAD20981	Human recombinant
C	49	26.6	22.0	495	21	AAA39492	Human APP intron,
C	50	26.6	22.0	581	22	AAI15643	Human breast canc
C	51	26.6	22.0	1062	9	AAH80667	Lambda SM2W3 encod

ALIGNMENTS

Corn

LF 1
 8574
 AAA48574 standard; cDNA; 2061 BP.
 AAA48574;
 19-SEP-2000 (first entry)
 cDNA encoding corn protein phosphatase 2A regulatory subunit A

Corn; protein phosphatase 2A; protein phosphorylation modulation, transgenic plant; gene therapy; ss.

Zea mays.

Key CDS	Location/Qualifiers
56..1820	Location/Qualifiers
/*tag="a	Location/Qualifiers
/product="protein phosphatase 2A regulatory subunit A"	Location/Qualifiers

XX		
PN	WO200036121-A2.	
XX		
PD	22-JUN-2000.	
XX		
PF	15-DEC-1999;	99WO-US29823
XX		

PR 16-DEC-1998; 98US-0112541.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Famodu OO, Miao G, Sakai H, Lee J, Rafalski JA, Klein TM.
XX
DR WPI: 2000-431599/37.
XX P-PSDB; AAV99819.
XX
PT Polynucleotides encoding plant protein phosphatase useful for
modulating reversible protein phosphorylation in plants -
XX
PS
XX
Claim 4; Page 53-54; 73pp; English.

The present sequence encodes corn protein phosphatase 2A regulatory subunit A. The sequence was identified in clone p0018.chsug10r.f15 of a cDNA library made from corn ear shoot. BLAST analysis showed that the present sequence encodes protein phosphatase 2A regulatory subunit A. The sequence may be used for the recombinant production of the protein in vivo, e.g. via a gene therapy protocol, or in vitro, e.g. in fermentation culture. The protein may then be used to modulate the process of reversible protein phosphorylation in plants. It may be used directly to supplement a plant's own production of the enzyme or to rectify mutations that result in the expression of inactive protein. The protein may also be used to test for modulators of protein phosphorylation which may be used to alter the activity of the enzyme.

Sequence 2061 BP; 549 A; 432 C; 498 G; 582 T; 0 other;

Query Match 100.0%; Score 121; DB 21; Length 2061;
Best Local Similarity 100.0%; Pred. No. 2,66-33;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Y 1 GTTTCCGTCGTACCTCGGTGACAGATGACGCGCTCCCATCTGATTAATGACGCGTCC 60
|||
DB 1908 GTTTCGCTGCTAGCTCGGTGACAGATGACGCGCTCCCATCTGATTAATGACGCGTCC 1967
|||
Y 61 TGATCCATTGTCGTTGTTTATTAATGTTGATTAATTAGACGACACACAGTACT 120
|||||
DB 1968 TGATCCATTGTCGTTGTTTATTAATGTTGATTAATTAGACGACACACAGTACT 2027
|||||
Y 121 T 121
|
DB 2028 T 2028

RESULT 2
ID AAA48576 standard; cDNA: 2604 BP.
XX
AC AAA48576;
XX
DT 19-SEP-2000 (first entry)
XX
DE cDNA encoding wheat protein phosphatase 2A regulatory subunit A.
XX
KW Wheat; protein phosphatase 2A; protein phosphorylation modulation;
transgenic plant; gene therapy; ss.
XX
OS Triticum aestivum.
XX
FH Key Location/Qualifiers
FT CDS 101..2028
FT /tag= a
FT /product= "protein phosphatase 2A regulatory
subunit A"
FT /note= "contains an intron"
FT exon 101..1537
FT /tag= b
FT /number= 1
FT intron 1538..1794
FT /tag= c
FT /number= 1

wheat

```

FT      exon      1795..2028
FT      /*tag=d
FT      /number=2
XX      PN      WO200036121-A2.
XX      PD      22-JUN-2000.
XX      PF      15-DEC-1999; 99WO-US29823.
XX      PR      16-DEC-1998; 98US-0112541.
XX      PA      (DUPO ) DU PONT DE NEMOURS & CO E. I.
XX      PL      Famodu OO, Miao G, Sakai H, Lee J, Rafalski JA, Klein TW;
XX      WPI: 2000-431599/37.
XX      DR      P-PSDB; AAV99821.
XX      PT      Polynucleotides encoding plant protein phosphatase useful for
XX      modulating reversible protein phosphorylation in plants -
XX      Claim 4; Page 59; 73pp; English.
XX      CC      The present sequence encodes wheat protein phosphatase 2A regulatory
XX      subunit A. The sequence was identified in clone wrl.pX0030.b10:fls of a
XX      cDNA library made from the root of a seven-day-old wheat seedling.
XX      BLAST analysis showed that the present sequence encodes protein
XX      phosphatase 2A regulatory subunit A. The sequence may be used
XX      for the recombinant production of the protein in vivo, e.g. via a gene
XX      therapy protocol, or in vitro, e.g. in fermentation culture. The protein
XX      may then be used to modulate the process of reversible protein
XX      phosphorylation in plants. It may be used directly to supplement a
XX      plant's own production of the enzyme or to rectify mutations that result
XX      in the expression of inactive protein. The protein may also be used to
XX      test for modulators of protein phosphorylation which may be used to
XX      alter the activity of the enzyme.
XX      SO      Sequence 2604 BP; 779 A; 515 C; 579 G; 731 T; 0 other:
XX
XX      Query Match      24.1%; Score 29.2; DB 21; Length 2604;
XX      Best Local Similarity 75.8%; Pred. No.2.9;
XX      Matches 50; Conservative 0; Mismatches 13; Indels 3; Gaps 1;
XX
XX      QY      38 CCATCGTGAATAAATGGACGGTCTGATCCAMTGTTCGTTGTTATTAATGTTGTAATAAT 97
XX      ||||||||| 1 ||||| 1 1 |||||||||||||||
XX      DB      2330 CCATCGTGAATAAATGGATGGGCTCTGTCCCTTT---TGTGTATTAATGTTGTAATAAT 2386
XX
XX      QY      98 TGAGCA 103
XX      |||||
XX      DB      2387 TGAGCA 2392
XX
XX      RESULT 3
XX      ID      ABO25086
XX      AC      ABO25086 standard; DNA: 705 BP.
XX      XX      ABO25086;
XX      DT      12-JUL-2002 (first entry)
XX
XX      DE      Oligonucleotide for detecting cytosine methylation SEQ ID NO 11677.
XX      KW      Human; cytosine methylation; 5'-CPG-3'; uracil; cytosine; diagnosis;
XX      drug; side effect; cancer; central nervous system; cardiovascular;
XX      gastrointestinal; respiratory system; single nucleotide polymorphism;
XX      SNP; cell differentiation; ds.
XX      OS      Homo sapiens.
XX      PN      WO200218632-A2.
XX      DT      07-MAR-2002.

```

```

XX 01-SEP-2001; 2001WO-EPI10074.
PF 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful
XX for diagnosis and prognosis, comprises selective hybridization of
XX amplicons from chemically treated DNA
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CPG-3', present in a
XX genomic sample of DNA. The sample is treated chemically to convert
XX cytosine (C) but not methylated C, to uracil, then part of the genomic
XX DNA that contains the target C is amplified to form a labeled amplicon.
XX The amplicon is hybridised to two classes, each with at least one
XX member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
XX and the degree of hybridisation to both classes is determined from the
XX label on the amplicon. From the ratio of labels hybridised to the two
XX classes of oligomers, the degree of methylation is calculated. The method
XX is used: (i) for diagnosis and/or prognosis of side effects of
XX therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
XX of the central nervous, cardiovascular, gastrointestinal and respiratory
XX systems etc., particularly by detecting mutations or single nucleotide
XX polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
XX types and for investigating cell differentiation. The method allows the
XX methylation status of many C residues to be determined simultaneously.
XX AB013410-AB034121 represent genomic DNA sequences used to illustrate the
XX method for determining the degree of cytosine methylation described in
XX the disclosure of the invention.
XX
XX Sequence 705 BP; 156 A; 73 C; 216 G; 260 T; 0 other;
XX
XX Query Match 23.8%; Score 28.8; DB 24; Length 705;
XX Best Local Similarity 58.0%; Pred. No. 2.5;
XX Matches 51; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
XX
XX Oy 26 GATCGACGCTGCCATGCTGATTAATGAGCGCTCCTGATCCATGTCGTTGTTATTA 85
XX ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 469 GATCGAGGTGGTATATTGTAATAGATGTTGATGATTCGTGCTGTTATATTTT 528
XX
XX Oy 86 ATGTTGTAATTAATTGAGCAGACACACA 113
XX || | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 529 TAGTATTGTTAAAGATGTGGCGCAATA 556
XX
XX RESULT 4
XX AB025087/c
XX ID AB025087 standard; DNA; 705 BP.
XX
XX AC AB025087;
XX
XX 12-JUL-2002 (first entry)
XX
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 11678.
XX
XX Human; cytosine methylation; 5'-CPG-3'; uracil; cytosine; diagnosis;
XX drug; side effect; cancer; central nervous system; cardiovascular;
XX gastrointestinal; respiratory system; single nucleotide polymorphism;
XX SNP; cell differentiation; ds.
XX
XX Homo sapiens.
XX
XX WO200218632-A2.
XX

```

```

PD 07-MAR-2002.
XX
XX 01-SEP-2001; 2001WO-EPI10074.
PF 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful
XX for diagnosis and prognosis, comprises selective hybridization of
XX amplicons from chemically treated DNA
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CPG-3', present in a
XX genomic sample of DNA. The sample is treated chemically to convert
XX cytosine (C) but not methylated C, to uracil, then part of the genomic
XX DNA that contains the target C is amplified to form a labeled amplicon.
XX The amplicon is hybridised to two classes, each with at least one
XX member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
XX and the degree of hybridisation to both classes is determined from the
XX label on the amplicon. From the ratio of labels hybridised to the two
XX classes of oligomers, the degree of methylation is calculated. The method
XX is used: (i) for diagnosis and/or prognosis of side effects of
XX therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
XX of the central nervous, cardiovascular, gastrointestinal and respiratory
XX systems etc., particularly by detecting mutations or single nucleotide
XX polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
XX types and for investigating cell differentiation. The method allows the
XX methylation status of many C residues to be determined simultaneously.
XX AB013410-AB034121 represent genomic DNA sequences used to illustrate the
XX method for determining the degree of cytosine methylation described in
XX the disclosure of the invention.
XX
XX Sequence 705 BP; 260 A; 216 C; 73 G; 156 T; 0 other;
XX
XX Query Match 23.8%; Score 28.8; DB 24; Length 705;
XX Best Local Similarity 58.0%; Pred. No. 2.5;
XX Matches 51; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
XX
XX Oy 26 GATCGACGCTGCCATGCTGATTAATGAGCGCTCCTGATCCATGTCGTTGTTATTA 85
XX ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 237 GATCGAGGTGGTATATTGTAATAGATGTTGATGATTCGTGCTGTTATATTTT 178
XX
XX Oy 86 ATGTTGTAATTAATTGAGCAGACACACA 113
XX || | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 177 TAGTATTGTTAAAGATGTGGCGCAATA 150
XX
XX RESULT 5
XX AAV64373
XX ID AAV64373 standard; cDNA; 1519 BP.
XX
XX AC AAV64373;
XX
XX 15-FEB-1999 (first entry)
XX
XX GABA-gated chloride channel TBW-a3 cDNA.
XX
XX TBW-a3; GABA-gated chloride channel; tobacco budworm; insecticide;
XX ss.
XX
XX Heliothis virescens.
XX
XX Key Location/Qualifiers
XX CDS 1..1446
XX /*tag= a
XX

```

CC This cDNA sequence encompasses the open reading frame encoding
CC GABA-gated chloride channel TBW-a3 (see AAM81635-36) of tobacco
CC budworm (*Heliothis virescens*). TBW-a3, TBW-a2 (see AAM81633-34)
CC and TBW-a1 (see AAM81637) proteins are 3 receptor isoforms that show
CC sequence homology to each other and to other insect GABA-gated
CC chloride channels. TBW-2a cDNA was obtained from *H. virescens* 4th
CC instar larva RNA by PCR and RACE amplifications. The invention
CC provides expression vectors in which a nucleic acid encoding a
CC GABA-gated chloride channel is driven by an inducible promoter, and
CC a claimed process for producing a GABA-gated chloride channel by
CC transformed cells. The GABA-gated channels or cells expressing
CC them can be used for characterizing a bioactive agent (claimed),
CC e.g. for use as an insecticide. Probes and primers that identify
CC or amplify GABA-gated chloride channel nucleic acids of the
CC invention are also claimed.

Matches 63; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

RESULT 6
ABV48454
ID ABV48454 standard; cDNA; 405 BP.

DT 17-SEP-2002 (first entry)

DE Human prostate expression marker CDNA 48445.

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker,
KW pharmacogenomic marker; gene; ss.
KW ...

OS Homo sapiens.

PI Schlegel R, Endege WO, Monahan JE;

DR WPI; 2001-662795/76.

PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -

PS Claim 1; Page 9499; 11750pp; English

CC The invention relates to an isolated nucleic acid molecule (1) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (1) is useful for:
CC (a) ascertaining whether a nation is afflicted with a disease;
CC (b) ascertaining whether a nation is afflicted with a disease.

(b) monitoring the progression of prostate cancer in a patient;

CC cancer in a patient;
CC (d) assessing the effectiveness of a tobacco cessation product in cancer patients.

CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC in a patient;

(9) determining whether prostate cancer has metastasized in a patient

CC (ii) assessing the aggressiveness of nodules or prostate cancer in a patient:

(1) is also useful as a pharmacodynamic or pharmacogenomic marker.

sequence 405 BP; 106 A; 86 C; 102 G; 111 T; 0 Clnet,

Query Match	23.6%	Score 28.6;	DB 23,	Length 405;
Best Local Similarity	59.0%;	Pred. No. 2.4;		
Matches 49;	Conservative 0;	Mismatches 34;	Indels 0;	Gaps 0;

9 TCTAGCCTCGGTGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCTCTGATCCAT 68

Db 321 TATAGCAGTGTCTCATCACCTTGGTGATGCTGAAGAAAAACCGTACCCATC 380

Qy	69	TGTCGTTGTGTTATTAATGTTG	91
Db	381	TCTTCATGTTGTGTTGGAAGTTG	403

RESULT	7
AAQ88698	
ID	AAQ88698 standard; cDNA to mRNA; 297 BP.

DT 11-NOV-1995 (first entry)

DE Beta-amyloid precursor protein C-terminal peptide mutant gene

KW Human; beta-amyloid precursor protein mutant; C-terminal peptide;

KW gene therapy; ss.

OS Homo sapiens

PN EP653154-A

```

XX 17-MAY-1995.
PD 07-NOV-1994; 94EP-0117512.
XX 12-NOV-1993; 93JP-0306026.
XX (FARH ) HOECHST JAPAN LTD.
PA (FARH ) HOECHST JAPAN KK.
XX Kawayabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
PI WPI: 1995-180492/24.
DR P-PSDB: AAR/4696.
XX
PT Transgenic animal model for Alzheimer's disease - contains DNA encoding
PT part of beta-amyloid precursor protein in a gene construct designed for
PT over-expression in various cell types
PS
XX Claim 2; Page 13-14; 32pp; English.
XX
CC The sequence encodes a human brain beta-amyloid precursor protein
CC (APP) mutant C-terminal peptide, and differs from AAQ88696 by
CC conversion of Val to Ile at codon 46. The DNA may be transferred
CC along with an APP signal peptide gene (e.g. AAQ88695) into somatic and
CC germ cells of a non-human mammal, and the resulting transgenic animal
CC may be used as a model for Alzheimer disease (AD). The animal model
CC exhibits symptoms similar to AD, producing large quantities of APP
CC C-terminal peptide, death of neuron cells in pyramidal cells at
CC cerebral amyloid regions, increases in glial cells and deposition
CC of abnormally phosphorylated tau protein. The animal model may
CC be used to develop new therapies for AD, including gene therapy
CC strategies.
XX
SQ Sequence 297 BP; 87 A; 64 C; 77 G; 69 T; 0 other;
XX
Query Match 23.3%; Score 28.2; DB 16; Length 297;
Best Local Similarity 59.3%; Pred. No. 3.1;
Matches 48; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 11 TAGCCTCGTGGACAGATCGACGCTGATTAATGAGCGGTCGATCCATTG 70
Db 122 TAGCGACAGTATCATCTACCTTGGTGTGATGCTGAGAGAAACAGTACATCCATTG 181
QY 71 TTCGTTGCTTATTATGTTG 91
Db 182 ATCATGTGTGTGTGAGGTTG 202
XX
RESULT 8
AAK9387
ID AAK9387 standard; DNA; 300 BP.
XX
AC AAK9387;
XX
DT 27-JUN-2002 (first entry)
XX
DE DNA of wild type C99 portion of human APP with the London mutation.
XX
KW Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;
KW amyloid precursor protein; tissue-specific expression control; human APP;
KW APP pathway modulator; gene therapy; mutant; ds.
XX
XX Homo sapiens.
XX OS
XX PN WO200226820-A2.
XX
PD 04-APR-2002.
XX
PF 01-OCT-2001; 2001WO-EP11345.
XX
PR 29-SEP-2000; 2000US-236893P.
PR 14-JUN-2001; 2001US-298309P.
XX

```

```

XX (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERN GES MBH.
XX
XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
PI Reinhardt MWM, Zisman S;
XX WPI: 2002-315796/35.
DR
XX
PT New transgenic fly, containing DNA encoding an Abeta portion of human
PT APP, useful for identifying agents which modulate the APP pathway and
PT which can be used to treat Alzheimer's disease -
XX
PS Claim 4; Page 84; 129pp; English.
XX
CC The invention relates to a transgenic fly whose genome comprises DNA
CC encoding a polypeptide having the Abeta portion of human amyloid
CC precursor protein (APP), fused to a signal sequence. The DNA sequence
CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
CC the specification. The DNA sequence is operably linked to a tissue-
CC specific expression control sequence. Expression of the sequence gives
CC the fly an altered phenotype. The purpose of the invention is for
CC identifying agents that inhibit or promote the expression and/or function
CC of genes or encoded polypeptides which modify the APP pathway. The agent
CC is a compound, tripe helix DNA, antisense oligonucleotide, double
CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
CC to treat conditions such as Alzheimer's disease. The agent can be used as
CC an APP pathway modulator or in gene therapy. This polynucleotide sequence
CC represents the DNA of the wild type C99 portion of human APP with the
CC London mutation of the invention.
XX
SQ Sequence 300 BP; 88 A; 65 C; 78 G; 69 T; 0 other;
XX
Query Match 23.3%; Score 28.2; DB 24; Length 300;
Best Local Similarity 59.3%; Pred. No. 3.1;
Matches 48; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 11 TAGCCTCGTGGACAGATCGACGCTGATTAATGAGCGGTCGATCCATTG 70
Db 122 TAGCGACAGTATCATCTACCTTGGTGTGATGCTGAGAGAAACAGTACATCCATTG 181
QY 71 TTCGTTGCTTATTATGTTG 91
Db 182 ATCATGTGTGTGTGAGGTTG 202
XX
RESULT 9
AAC79021
ID AAC79021 standard; DNA; 1357 BP.
XX
AC AAC79021;
XX
DT 14-FEB-2001 (first entry)
XX
DE Human secreted protein gene 25 clone HODAH24.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatoprotective; antidiabetic; antiinflammatory; antitumor;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; ss.
XX
XX Homo sapiens.
XX OS
XX PN WO200058358-A1.
XX
PD 05-OCT-2000.
XX
PF 23-MAR-2000; 2000WO-US07725.
XX
PR 26-MAR-1999; 99US-0126602.
PR 14-JAN-2000; 2000US-0176063.
XX

```

PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Komatsoulis G;
 XX
 DR WPI: 2000-594640/56.
 DR P-PSDB: AAB44359.
 XX
 PT Fourty nine nucleic acid molecules encoding human secreted proteins,
 PT useful in the prevention, treatment and diagnosis of cancer, immune
 PT disorders, cardiovascular disorders and neurological diseases -
 XX
 PS Claim 1: Page 327-328; 367pp; English.
 XX
 CC The invention relates to the isolation of genes AHC78997-C79045 encoding
 CC 49 human secreted proteins AAB4435-B44382. The genes can be used to
 CC generate fusion proteins by linking to the gene for the human
 CC immunoglobulin G Fc portion (AHC78988) for increasing the stability of
 CC the fusion protein as compared to the human protein only. The genes and
 CC proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated
 CC from a range of human tissues disclosed in the specification. The
 CC nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)
 CC wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 XX
 SQ Sequence 1357 BP; 386 A; 272 C; 299 G; 398 T; 2 other:
 XX
 Query Match 23.1%; Score 28; DB 21; Length 1357;
 Best Local Similarity 52.6%; Pred. No. 6.1;
 Matches 61; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
 OY 1 GTTTTCGCTAGCCTGGTGGACAGATGACGCTGCCATGCTGTAATAATGACGCTCC 60
 DB 871 GTTACCTTTGTGACGTGATCCACCCACCTGGCTCCCAAGTGTGATTAACAGACG 930
 OY 61 TGATCCATGTTGCTGTGTATATATGTTGATATATAGACGACACACACGT 116
 DB 931 TGAGCCATGTCGCCCGCATTTTAAATTTTAAATTTTAAATTAATTGCCACACCT 986
 RESULT 10
 ABL04431/C
 ID ABL04431 standard; cDNA; 1086 BP.
 XX
 AC ABL04431;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7775.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.

XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 DR P-PSDB: ABB60328.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1; SEQ ID NO 7775; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABB57737-ABB72072).
 CC (ABB57737-ABL16175) and the encoded proteins
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1086 BP; 295 A; 267 C; 273 G; 251 T; 0 other:
 XX
 Query Match 22.8%; Score 27.6; DB 23; Length 1086;
 Best Local Similarity 60.8%; Pred. No. 7.9;
 Matches 45; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 OY 36 GCCCATGCTGAATAATGACGCTCCTGATCCATGTTGCTGTATTATGTTGATA 95
 DB 943 GCCCATATCCGTAACGTGAGAGTCCCTCCGTAGGACGTTATCCGCTAGTAATAAA 884
 OY 96 ATTGACGACGACAC 109
 DB 883 ATTGATCGACACC 870
 RESULT 11
 ABL04430
 ID ABL04430 standard; cDNA; 3205 BP.
 XX
 AC ABL04430;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7772.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 DR P-PSDB: ABB60327.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

PS	xx	Claim 1; SEQ ID NO 7772; 21np + Sequence Listing; English.
CC	xx	The invention relates to an isolated nucleic acid detection reagent
CC	xx	capable of detecting 1000 or more genes from Drosophila. The invention is
CC	xx	useful in developmental biology and in elucidating cell signalling and
CC	xx	cell-cell interactions in higher eukaryotes for the development of
CC	xx	insecticides, therapeutics and pharmaceutical drugs. The invention
CC	xx	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC	xx	sequences (ABL01840-ABL16175) and the encoded proteins
CC	xx	(AB857737-AB872072).
CC	xx	The sequence data for this patent did not form part of the printed
CC	xx	specification, but was obtained in electronic format directly from WIPO
CC	xx	at ftp.wipo.int/pub/published_pcr_sequences.
SO	xx	Sequence 3205 BP; 932 A; 681 C; 655 G; 937 T; 0 other;
Qy	xx	Query Match 22.8%; Score 27.6; DB 23; Length 3205;
Db	xx	Best Local Similarity 60.8%; Pred. No. 12;
Matches	45; Conservative 0; Mismatches 29; Indels 0; Gaps 0	
Qy	36	GCCCATGCTGTAATAATGAGCGTCTCGATCCATTGTTCGTGTATTAATGTTCTATA 95
Db	1199	GCCCATATTCGGAATGAGGGTCCCTCCGTAGACGTTATTCGCGCTAGGTATATAA 1258
Qy	96	ATTGAGCAGAGCACC 109
Db	1259	ATTGATCAGACACC 1272
RESULT 12		
ABL04426		
ID	ABL04426	standard; cDNA; 3457 BP.
AC	xx	ABL04426;
XX	xx	
XX	xx	26-MAR-2002 (first entry)
DE	xx	Drosophila melanogaster expressed polynucleotide SEQ ID NO. 7760.
XX	xx	
KW	xx	Drosophila; developmental biology; cell signalling; insecticide;
XX	xx	pharmaceutical; gene; ss.
OS	xx	Drosophila melanogaster.
PN	xx	WO200171042-A2.
PD	xx	29-SEP-2001.
PE	xx	23-MAR-2001; 2001WO-US09231.
XX	xx	
PR	xx	23-MAR-2000; 2000US-191637P.
XX	xx	
XX	xx	11-JUL-2000; 2000US-0614150.
PA	xx	(PEKE) PE CORP NY.
PI	xx	Venter JC, Adams M, Li PWD, Myers EW;
DR	xx	WPI: 2001-656860/75.
DR	xx	P-PSDB; ABB60323.
PT	xx	New isolated nucleic acid detection reagent for detecting 1000 or more
PT	xx	genes from Drosophila and for elucidating cell signalling and cell-cell
PT	xx	interactions -
PS	xx	Claim 1; SEQ ID NO 7760; 21np + Sequence Listing; English.
CC	xx	The invention relates to an isolated nucleic acid detection reagent
CC	xx	capable of detecting 1000 or more genes from Drosophila. The invention is
CC	xx	useful in developmental biology and in elucidating cell signalling and
CC	xx	cell-cell interactions in higher eukaryotes for the development of
CC	xx	insecticides, therapeutics and pharmaceutical drugs. The invention
CC	xx	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

```

CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
CC
XX
SQ Sequence 3457 BP; 895 A; 779 C; 690 G; 1093 T; 0 other;

Query Match 22.8%, Score 27.6; DB 23; Length 3457;
Best Local Similarity 60.8%; Pred. No. 12;
Matches 45; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 36 GCCCATGCTGAATTAATGAGCGGCTCTGATCCATGTTGTTGTTATTAATGTTGATA 95
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 3299 GCCCATATCCGTAACATGAGAGGCTCCCTCCCTAGGACGTTATTCGGCTAGATATAAA 3358
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 96 ATTGAGCAGACAC 109
    |||||  |||||  |||||
Db 3359 ATTGATCAGACACC 3372
    |||||  |||||  |||||

RESULT 13
ABL29895/c
ID ABL29895 standard; DNA; 4659 BP.
AC
XX ABL29895;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 41158.
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
XX
XX pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PMD, Myers EW;
XX
XX WPI: 2001-656860/75.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Claim 1; SEQ ID NO 41158; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA
XX sequences (ABB57737-ABB72072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4659 BP; 1472 A; 1196 C; 1153 G; 838 T; 0 other;

Query Match 22.6%; Score 27.4; DB 23; Length 4659;
Best Local Similarity 69.8%; Pred.No. 16;

```

[illegible]

XX	Human CARD-4 DNA.	
DE		
XX		
KW	CARD-3; caspase recruitment domain; CARD-4; regulation; detection;	
KW	caspase activation; detection; screening; therapy; diagnosis; disease;	
KW	apoptotic cell death; Fas/APo-1 receptor complex; TNF receptor complex;	
KW	cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection;	
KW	hormone-dependent tumor; autoimmune disorder; Alzheimer's disease;	
KW	systemic lupus erythematosus; immune-mediated glomerulonephritis; stroke;	
KW	Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;	
KW	sphal muscular dystrophy; cerebellar degeneration; anaemia; drug;	
KW	myelodysplastic syndrome; myocardial infarction; cell proliferation;	
KW	cell differentiation; cell survival; CARD-4L; CARD-4S; CARD-4Y;	
KW	CARD-4Z; human; ds.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	exon	364..685
FT		/*tag= a
FT		/number= 1
FT		485..31768
FT	CDS	/*tag= b
FT		/product= "CARD-4"
FT		686..2094
FT	intron	/*tag= c
FT		/number= 1
FT		2095..2269
FT	exon	/*tag= d
FT		/number= 2
FT		2270..4365
FT	intron	/*tag= e
FT		/product= 2
FT		4366..6190
FT	exon	/*tag= f
FT		/number= 3
FT		6191..9024
FT	intron	/*tag= g
FT		/number= 3
FT		9025..9108
FT	exon	/*tag= h
FT		/product= 4
FT		9109..10355
FT	intron	/*tag= i
FT		/number= 4
FT		10356..10439
FT	exon	/*tag= j
FT		/number= 5
FT		10440..11181
FT	intron	/*tag= k
FT		/number= 5
FT		11182..11265
FT	exon	/*tag= l
FT		/number= 6
FT		11266..19749
FT	intron	/*tag= m
FT		/number= 6
FT		19750..19833
FT	exon	/*tag= n
FT		/number= 7
FT		19834..21324
FT	intron	/*tag= o
FT		/number= 7
FT		21325..21408
FT	exon	/*tag= p
FT		/number= 8
FT		21409..24226
FT	intron	/*tag= q
FT		/number= 8
FT		24227..24310
FT	exon	/*tag= r
FT		/number= 9
FT		24311..27948
FT	intron	

[illegible]

ID	AA140765	standard; DNA; 32042 BP.
XX	AA140765	
AC	AA140765	
XX	AA140765	
DT	27-SEP-2002	(first entry)
XX	27-SEP-2002	(first entry)
DE	Genomic DNA of human CARD-4 SEQ ID NO 44.	
XX	Genomic DNA of human CARD-4 SEQ ID NO 44.	
KM	Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimers;	
KM	cerebroprotective; antiparkinsonian; antischleotic; ophthalmological;	
KM	neotropic; antianemic; Caspase Recruitment Domain; CARD; CARD-4L; p53;	
KM	cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder;	
KM	hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer;	
KM	systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease;	
KM	anemia; neutropenia; myelodysplastic syndrome; human; ds.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	US6369196-B1.	
PN	US6369196-B1.	
XX	09-APR-2002.	
PD	09-APR-2002.	
XX	05-FEB-1999; 99US-0245281.	
PF	05-FEB-1999; 99US-0245281.	
XX	06-FEB-1998; 98US-0019942.	
PR	17-JUN-1998; 98US-0099041.	
XX	08-DEC-1998; 98US-0207359.	
PR	08-DEC-1998; 98US-0207359.	
XX	(MILL-) MILLENNIUM PHARM INC.	
PA	(MILL-) MILLENNIUM PHARM INC.	
XX	Bertin J;	
PI	Bertin J;	
XX	WPI: 2002-391988/42.	
DR	WPI: 2002-391988/42.	
XX	Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and	
PT	CARD-4S) useful for diagnosing and treating e.g. Parkinson's and	
PT	Alzheimer's disease, cancers and viral infections	
XX	Disclosure; Fig 18; 116pp; English.	
PS	Disclosure; Fig 18; 116pp; English.	
XX	The invention relates to novel isolated Caspase Recruitment Domain (CARD)	
XX	polypeptides. CARD-4L and CARD-4S. The CARD proteins of the invention may	
CC	be used to treat disorders associated with decreased CARD expression by	
CC	supplementing the patient's own production of CARD. Disorders associated	
CC	with the expression and activity of CARD include cancers (particularly	
CC	follicular lymphomas, carcinomas associated with mutations in p53, and	
CC	hormone-dependent tumours such as breast cancer, prostate cancer, and	
CC	ovarian cancer), autoimmune disorders (such as systemic lupus	
CC	erythematosus, immune-mediated glomerulonephritis), viral infections	
CC	(such as those caused by herpes viruses, poxviruses, and adenoviruses),	
CC	neurological diseases (such as Alzheimer's disease, Parkinson's	
CC	disease, amyotrophic lateral sclerosis (ALS) retinitis pigmentosa,	
CC	spinal muscular atrophy, and various forms of cerebellar degeneration),	
CC	anaemia associated with chronic disease, aplastic anaemia, chronic	
CC	neutropenia, and the myelodysplastic syndromes. This polynucleotide	
CC	sequence represents the DNA of a human CARD relating to the invention.	
XX	Sequence 32042 BP; 7389 A; 7540 C; 7721 G; 9392 T; 0 other;	
SQ	Sequence 32042 BP; 7389 A; 7540 C; 7721 G; 9392 T; 0 other;	
XX	Query Match 22.6%; Score 27.4; DB 24; Length 32042;	
XX	Best Local Similarity 62.3%; Pred No. 30;	
XX	Matches 43; Conservative 0; Mismatches 26; Indels 0; Gaps 0	
OY	28 TCGACGCTGCCATGCTGATTAATGACGCGTCTGCATTCATTTGCTGTGATTAAAT 87	
DB	18335 TTGACATACCCACCTCAATAGAGTGTGAGCTCTCATTTGGTTGATCTCTGAC 18394	
OY	88 GTTGTATTA 96	
DB	18395 GCTTTTAA 18403	

RESULT 18
ABO25024
ID ABO25024 standard; DNA: 628 BP.
XX
AC ABO25024;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 11615.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABO13410-ABO54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 628 BP; 161 A; 54 C; 160 G; 253 T; 0 other;

Query Match 22.3%; Score 27; DB 24; Length 628;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 45; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

OY 26 GATCGACGCTGCCATGCTGATTAATGACGCTCCTGATCCATTTGCTGTATTATTA 85
DB 509 GATCGACGCTGCTATTTGTTAATGATGATGATGATGATGATGATGATGATTTT 568
OY 86 ATGTTGATTAATTGA 100
DB 569 TAGTATTTGTTAACGA 583

RESULT 19
ABO25025/C
ID ABO25025 standard; DNA: 628 BP.
XX
AC ABO25025;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 11616.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABO13410-ABO54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 628 BP; 253 A; 160 C; 54 G; 161 T; 0 other;

Query Match 22.3%; Score 27; DB 24; Length 628;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 45; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

OY 26 GATCGACGCTGCCATGCTGATTAATGACGCTCCTGATCCATTTGCTGTATTATTA 85
DB 120 GATCGACGCTGCTATTTGTTAATGATGATGATGATGATGATGATGATGATTTT 61
OY 86 ATGTTGATTAATTGA 100
DB 60 TAGTATTTGTTAACGA 46

RESULT 20
ABV54453
ID ABV54453 standard; cDNA; 374 BP.
XX
AC ABV54453;
XX
DT 17-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 54444.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer; useful
PT for detecting presence of prostate cancer; stage of prostate cancer
XX
PS Claim 1; Page 10526; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (1) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (1) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 374 BP; 95 A; 109 C; 80 G; 90 T; 0 other;
XX
Query Match 22.1%; Score 26.8; DB 23; Length 374;
Best Local Similarity 61.4%; Pred. No. 11;
Matches 43; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
XX
OY 21 GGACAGATCGACGCTCCATGCTGATTAATGAGCGCTCCATGCTTGTGTGT 80
DB 275 GAACAGACCTACGATCTTCCGATTAACAGCTCCGATCAATCTCAGTTCCAC 334
OY 81 TATTAATGTT 90
DB 335 TCTAATGCT 344

RESULT 21
AAI86054
ID AAI86054 standard; cDNA; 408 BP.
XX
AC AAI86054;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide seq ID NO 6114.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN MO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
XX
DR P-PSDB: AAO06123.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukemia, inflammation and immune
PT disorders
XX
PS Claim 1; SEQ ID NO 6114; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, hematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 408 BP; 142 A; 55 C; 89 G; 121 T; 1 other;
XX
Query Match 22.1%; Score 26.8; DB 22; Length 408;
Best Local Similarity 59.0%; Pred. No. 11;
Matches 46; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
XX
OY 44 TGAATAAGAGAGCGCTCCATGCTGCTGATTAATGTTGATTAATGACCA 103
DB 209 TAAAGAGAGAGAGAGAGAGAAATGATGTTGCTTGTGTTAATTAATACCA 268
OY 104 GGACACAAACGCTAGCTT 121
DB 269 GCACCTTTTAAGTAAGTT 286
XX
RESULT 22
AAZ97380/C
ID AAZ97380 standard; cDNA; 486 BP.
XX

AC AA297380;
XX 18-APR-2000 (first entry)
XX
XX
DE Human prostate cancer differentially expressed gene #241.
XX
XX Prostate cancer specific gene; cancer; tumour progression; diagnose;
KW hyperproliferative cell growth; prostatic disorder; treatment;
KW metastatic prostate cancer; benign prostate hyperplasia; BPH; ss.
XX
OS Homo sapiens.
XX
XX WO9964594-A2.
XX
XX 16-DEC-1999.
XX
XX 10-JUN-1999; 99WO-US3181.
XX
XX 11-JUN-1998; 98US-0088877.
PR 09-JUN-1999; 99US-0088877.
XX
XX (CHIR) CHIRON CORP.
PA
XX Astel JH, Carroll E, Endege WO, Ford DM, Monahan JE, Schlegel R;
PI Steimann KE, Zhang J;
XX
XX WPI; 2000-116541/10.
DR
XX
XX
PT New isolated prostate cancer specific nucleic acids, used to develop
PT products for the diagnosis and treatment of cancer -
XX
XX Claim 2; Page 173; 212pp; English.
PS
XX This sequence represents a prostate cancer specific nucleic acid
CC sequence. The invention relates to a method for diagnosing cancer,
CC tumour progression, hyperproliferative cell growth or accompanying
CC biological and physical manifestations. The method involves contacting
CC the biological sample with a probe that comprises a sequence capable of
CC hybridising to any of the 339 nucleotide sequences given in the
CC specification (see AA297140-297478) and detecting duplex formation. The
CC products and methods of the invention can be used for the diagnosis,
CC prognosis, and treatment of cancer, tumour progression,
CC hyperproliferative cell growth, and accompanying physical and biological
CC manifestations. They can be used particularly for prostatic disorders
CC such as metastatic prostate cancer, localised prostate cancer, or benign
CC prostate hyperplasia (BPH).
XX
XX Sequence 486 BP; 137 A; 111 C; 128 G; 108 T; 2 other;
SQ
Query Match 22.1%; Score 26.8; DB 21; Length 486;
Best Local Similarity 59.0%; Pred. No. 12;
Matches 46; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
OY 33 GCTGCCCATGCTGATTAATGACGCTCCTGATCCATTGCTTGTGTTATTAATGTTCT 92
DB 303 GCTTCCCTAACTGCTGGAATTACAGTCTGACCACTGCTGCTCATTAATAACTTTT 244
OY 93 ATAATTGACGACGACACA 110
DB 243 AATTCATCACAATTACA 226
RESULT 23
AA297180/C
ID AA297180 standard; CDNA; 1004 BP.
XX
XX AA297180;
XX
XX 18-APR-2000 (first entry)
XX
XX Human prostate cancer differentially expressed gene #41.
XX
XX Prostate cancer specific gene; cancer; tumour progression; diagnose;
KW

KW hyperproliferative cell growth; prostatic disorder; treatment;
KW metastatic prostate cancer; benign prostate hyperplasia; BPH; ss.
XX
XX
OS Homo sapiens.
XX
XX WO9964594-A2.
XX
XX 16-DEC-1999.
XX
XX 10-JUN-1999; 99WO-US3181.
XX
XX 11-JUN-1998; 98US-0088877.
PR 09-JUN-1999; 99US-0088877.
XX
XX (CHIR) CHIRON CORP.
PA
XX Astel JH, Carroll E, Endege WO, Ford DM, Monahan JE, Schlegel R;
PI Steimann KE, Zhang J;
XX
XX WPI; 2000-116541/10.
DR
XX
XX
PT New isolated prostate cancer specific nucleic acids, used to develop
PT products for the diagnosis and treatment of cancer -
XX
XX Claim 2; Page 89; 212pp; English.
PS
XX This sequence represents a prostate cancer specific nucleic acid
CC sequence. The invention relates to a method for diagnosing cancer,
CC tumour progression, hyperproliferative cell growth or accompanying
CC biological and physical manifestations. The method involves contacting
CC the biological sample with a probe that comprises a sequence capable of
CC hybridising to any of the 339 nucleotide sequences given in the
CC specification (see AA297140-297478) and detecting duplex formation. The
CC products and methods of the invention can be used for the diagnosis,
CC prognosis, and treatment of cancer, tumour progression,
CC hyperproliferative cell growth, and accompanying physical and biological
CC manifestations. They can be used particularly for prostatic disorders
CC such as metastatic prostate cancer, localised prostate cancer, or benign
CC prostate hyperplasia (BPH).
XX
XX Sequence 1004 BP; 266 A; 208 C; 218 G; 259 T; 53 other;
SQ
Query Match 22.1%; Score 26.8; DB 21; Length 1004;
Best Local Similarity 59.0%; Pred. No. 15;
Matches 46; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
OY 33 GCTGCCCATGCTGATTAATGACGCTCCTGATCCATTGCTTGTGTTATTAATGTTCT 92
DB 299 GCTTCCCTAACTGCTGGAATTACAGTCTGACCACTGCTGCTCATTAATAACTTTT 240
OY 93 ATAATTGACGACGACACA 110
DB 239 AATTCATCACAATTACA 222
RESULT 24
AAD03458
ID AAD03458 standard; DNA; 2033 BP.
XX
XX AAD03458;
XX
XX 13-JUN-2001 (first entry)
XX
XX Zea mays modified ubiquitin regulatory system (mURS) DNA.
XX
XX Maize; modified ubiquitin regulatory system; mURS; heatshock element;
KW transgenic plant; gene regulation; ds.
XX
XX Zea mays.
XX
XX
XX Key Location/Qualifiers
FH misc-feature 718..723
FT /*tag= a

```

FT      /label="Kpn1-site"
FT      /note="Replaces the overlapping heatshock elements
XX      in the wild-type URS"
PN      WO200118220-A1.
XX
PD      15-MAR-2001.
XX
PF      07-SEP-2000; 2000WO-EP08690.
XX
PR      09-SEP-1999; 99EP-0307158.
XX
PA      (MONS ) MONSANTO PLC.
XX
PI      Goldsbrough A;
XX
DR      WPI: 2001-235203/24.
XX
PT      DNA sequence comprising a ubiquitin regulatory system, which lacks
PT      heatshock elements or is not heat inducible, useful for transforming
PT      plants (e.g. corn, wheat or barley) and regulating the expression of a
PT      structural gene under its control.
XX
PS      Claim 4; Fig 3; 39pp; English.
XX
CC      The present sequence is Zea mays modified ubiquitin regulatory system
CC      (MURS) DNA which lacks heatshock elements or is not heat inducible.
CC      The MURS DNA sequence is useful for transforming cells, particularly
CC      plant cells and creating transgenic plants. It is useful for regulating
CC      the expression of a structural gene, particularly when stressed with
CC      elevated temperature. The expression of associated DNA sequences, which
CC      is mediated by the present ubiquitin regulatory system, in transformed
CC      plant cells is stable and not influenced by environmental changes in
CC      temperature, which would normally affect expression mediated by a
CC      non-modified system.
XX
SQ      Sequence 2033 BP; 488 A; 424 C; 423 G; 698 T; 0 other:
XX
Query Match      22.1%; Score 26.8; DB 22; Length 2033;
Best Local Similarity 53.9%; Pred. No. 19;
Matches 55; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
XX
OY      3 TTTCGCTAGCCTCGTGACAGATCGACGCGTCCCATGCTGATTAATGACGCTCCTG 62
DB      1493 TATCGATCTAGCATAGTATGATCTGTTGATCGCGGTTTACTGATGATATACAGAGATG 1552
OY      63 ATCCATTGTTGCTGTTGTTATTAATGTTGTAATTAATGACAG 104
DB      1553 CTTTGTTCGCTGTTGTTGATGATGCTGTGTTGGCGG 1594
XX
RESULT 25
AAZ99961
ID      AAZ99961 standard; DNA; 2037 BP.
XX
AC      AAZ99961;
XX
DT      25-JUL-2000 (first entry)
XX
DE      Nucleotide sequence of a cloned fragment of p97-U3.
XX
KW      Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; SBEII-2;
KW      gelatinisation onset; transgenic plant; foodstuff; bakery product; ds.
XX
OS      Zea mays.
XX
PN      WO200015810-A1.
XX
PD      23-MAR-2000.
XX
PF      09-SEP-1999; 99WO-GB03011.
XX
PR      10-SEP-1998; 98EP-0307337.

```

```

XX      (PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.
PA      Goldsbrough A, Colliver S;
XX
DR      WPI: 2000-271446/23.
XX
PT      DNA encoding wheat starch branching enzyme II isoforms, useful in
PT      altering the characteristics of a plant, especially elevated starch
PT      gelatinization onset and/or peak temperature.
XX
PS      Disclosure; Fig 29; 197pp; English.
XX
CC      The present sequence represents a cloned fragment of p97-U3, which
CC      is used in the course of the invention. The specification describes novel
CC      subclasses of wheat starch branching enzyme II (SBEII), designated
CC      SBEII-1 and SBEII-2. The SBEII-1 genes are thought to have similar
CC      functional properties to the maize SBEIIb gene. Starch branching enzymes
CC      catalyse the formation of the alpha-1,6 linkages, creating branch points
CC      in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage
CC      followed by reattachment of the released alpha-1,4-glucan chain to the
CC      same or another glucosyl chain. SBEII polypeptides can be used to alter
CC      the characteristics of a plant, in particular to alter starch so that
CC      it has an elevated gelatinisation onset and/or peak temperature. Starch
CC      obtained from transgenic plants is useful in the preparation or
CC      processing a foodstuff, particularly bakery products.
XX
SQ      Sequence 2037 BP; 488 A; 426 C; 423 G; 700 T; 0 other:
XX
Query Match      22.1%; Score 26.8; DB 21; Length 2037;
Best Local Similarity 53.9%; Pred. No. 19;
Matches 55; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
XX
OY      3 TTTCGCTAGCCTCGTGACAGATCGACGCGTCCCATGCTGATTAATGACGCTCCTG 62
DB      1495 TATCGATCTAGCATAGTATGATCTGTTGATCGCGGTTTACTGATGATATACAGAGATG 1554
OY      63 ATCCATTGTTGCTGTTGTTATTAATGTTGTAATTAATGACAG 104
DB      1555 CTTTGTTCGCTGTTGTTGATGATGCTGTGTTGGCGG 1596
XX
RESULT 26
AAH14585/C
ID      AAH14585 standard; cDNA; 2650 BP.
XX
AC      AAH14585;
XX
DT      26-JUN-2001 (first entry)
XX
DE      Human cDNA sequence SEQ ID NO:12185.
XX
KW      Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS      Homo sapiens.
XX
PN      EP1074617-A2.
XX
PD      07-FEB-2001.
XX
PF      28-JUL-2000; 2000EP-0116126.
XX
PR      29-JUL-1999; 99JP-0248036.
XX
PR      27-AUG-1999; 99JP-0300253.
XX
PR      11-JAN-2000; 2000JP-0118776.
XX
PR      02-MAY-2000; 2000JP-0183767.
XX
PR      09-JUN-2000; 2000JP-0241899.
XX
PA      (HELI-) HELIX RES INST.
XX
PI      Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX      Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

```


[illegible]

PA	(HELI-)HELIX RES INST.
PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PJ	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
PK	WPI, 2001-318749/34.
PL	Primer sets for synthesizing polynucleotides, particularly the 5602
PM	full-length cDNAs defined in the specification, and for the detection
PN	and/or diagnosis of the abnormality of the proteins encoded by the
PO	full-length cDNAs -
PP	Claim 8; SEQ ID 15232; 2537np + CD ROM; English.
PS	The present invention describes primer sets for synthesising 5602
PT	full-length cDNAs defined in the specification. Where a primer set
PV	comprises: (a) an oligo-dr primer and an oligonucleotide complementary
PW	to the complementary strand of a polynucleotide which comprises one of
PX	the 5602 nucleotide sequences defined in the specification, where the
PY	oligonucleotide comprises at least 15 nucleotides; or (b) a combination
PZ	of an oligonucleotide comprising a sequence complementary to the
QA	complementary strand of a polynucleotide which comprises a 5'-end
QB	sequence and an oligonucleotide comprising a sequence complementary to a
QC	polynucleotide which comprises a 3'-end sequence, where the
QD	oligonucleotide comprises at least 15 nucleotides and the combination of
QE	the 5'-end sequence/3'-end sequence is selected from those defined in
QF	the specification. The primer sets can be used in antisense therapy and
QG	in gene therapy. The primers are useful for synthesising polynucleotides,
QH	particularly full-length cDNAs. The primers are also useful for the
QI	detection and/or diagnosis of the abnormality of the proteins encoded by
QJ	the full-length cDNAs. The primers allow obtaining of the full-length
QK	cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
QL	AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
QM	AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
QN	represent oligonucleotides, all of which are used in the exemplification
QO	of the present invention.
QP	Sequence 2897.BP; 882 A; 564 C; 696 G; 755 T; 0 other;
QQ	
QR	Query Match 22.1%; Score 26.8; DB 22; Length 2897;
QS	Best Local Similarity 59.0%; Pred. No. 22;
QT	Matches 46; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QU	
QV	33 GCTGCCCATGCTGATAAATGCAGCGTCCTGATCCATTGGTGTGTTAATATGTTGT 92 DB 2080 GCTTCCTAAACGTGCGGATTTACAGTCTCGAGCCACTGTGCTCCTCAATAAACTTTT 2021
QW	93 ATAATTGAGCAGACACA 110
QX	Db 2020 AATTCATCACACATTACA 2003
QY	
QZ	RESULT 28
RA	AAFT31290/C
RB	ID AAT31290 standard; CDNA: 3095 BP.
RC	XX AAT31290;
RD	XX
RE	XX 24-FEB-1997 (first entry)
RF	XX
RG	DE Mouse poly-immunoglobulin receptor, CDNA.
RH	XX
RI	KW Mouse; immunoglobulin; receptor; protection protein; mutants;
RJ	KW heavy chain; antigen binding domain; protection; pathogen;
RK	KW mucosal; environment; gastrointestinal; passive; immunisation;
RL	KW Guy's 13 antibody; prevention; dental caries; Streptococcus;
RM	KW poly; sorbinus; murine; ss.
RN	XX
RO	OS Mus musculus.
RP	XX
RQ	Key Location/Qualifiers
RS	CDS 85..2400
RT	/ftag= a
RU	FT

```

XX XX WO9621012-A1.
XX PN
XX PD 11-JUL-1996.
XX XX
PF 27-DEC-1995: 95MO-US16689.
XX XX
XX XX 04-MAY-1995: 95US-0434000.
XX PR 30-DEC-1994: 94US-0367395.
XX XX
PA (PLAN-) PLANT BIOTECHNOLOGY INC.
PA (UNNE-) UNITED MEDICAL & DENTAL SCHOOLS GUYS.
PA (PLAN-) PLANET BIOTECHNOLOGY INC.
PI Hiatt AC, Lehner T, Ma JKC;
XX XX
XX DR WPI: 1996-333987/33.
XX DR P-PSDB: AAM03180.
XX XX
XX PT Immunoglobulin and protection protein complex and its prodn. in
XX PT plants - useful for passive immunisation against mucosal antigens,
XX PT esp. against S. mutans and S. sorbinus to prevent dental caries
XX PS
XX PS Disclosure: Pages 117-121; 152pp; English.
XX CC
XX CC The present sequence encodes the mouse poly-immunoglobulin (Ig)
XX CC receptor, a portion of which corresp. to residues 1-627, pref:
XX CC 1-606, or esp. residues 13-45, 1-120, 110-230, 210-340, 320-450,
XX CC 440-550, 550-606 or 550-627 comprises a protection protein (PP).
XX CC The Ig of the invention comprises a PP as above in association with
XX CC an Ig derived heavy chain, having at least a portion of an antigen
XX CC (Ag) binding domain. The PP protects the Ig in harsh mucosal, e.g.
XX CC gastrointestinal, environments, therefore enhancing its
XX CC effectiveness in passively immunising animals against mucosal
XX CC pathogens. The Ag binding domain is specifically derived from the
XX CC Guy's 13 antibody, and the Ig can be used to prevent dental caries
XX CC by binding, e.g. Streptococcus mutans serotypes C, e and f, or
XX CC S. sorbinus serotypes d and g.
XX SQ
XX SQ Sequence 3095 BP; 861 A; 796 C; 784 G; 654 T; 0 other;
XX
XX Query Match 22.1%; Score 26.8; DB 17; Length 3095;
XX Best Local Similarity 64.5%; Pred. No. 22;
XX Matches 40; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
XX
XX QY 30 GACGCTGCCATGCTGATAAATGAGCGTCTGATTCATTTGTTTATTAATGT 89
XX ID 111 111 111 111 111 111 111 111 111 111 111 111
XX DB 760 GACCTTCTCCAGCTTGCGAGATGTACAGCCACATCATTTGCTGTAGTACTAATGT 701
XX
XX QY 90 TG 91
XX ID 11
XX DB 700 TG 699
XX
XX RESULT 29
XX ABL1634/c
XX ID ABL1634 standard; DNA; 13255 BP.
XX
XX AC ABL1634;
XX
XX DT 26-MAR-2002 (first entry)
XX
XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1375.
XX XX
XX XX Drosophila: developmental biology; cell signalling; insecticide;
XX XX pharmaceutical; gene; ds.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX

```

```

PF 23-MAR-2001; 2001WO-US09231.
XX XX
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX XX
XX PA (PEKE ) PE CORP NY.
XX XX
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI: 2001-656860/75.
XX XX
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX PS
XX PS Claim 1; SEQ ID NO 1375; 21pp + Sequence Listing; English.
XX CC
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABB57737-ABB72072) and the encoded proteins
XX CC (ABB57737-ABB72072).
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pcr_sequences.
XX SQ
XX SQ Sequence 13255 BP; 3879 A; 2652 C; 2622 G; 4102 T; 0 other;
XX
XX Query Match 22.1%; Score 26.8; DB 23; Length 13255;
XX Best Local Similarity 61.4%; Pred. No. 37;
XX Matches 43; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
XX
XX QY 44 TGATAATGAGCGCTCGATTAATGCTGTTGTTATTAATGTTATTAATGACCA 103
XX ID 11111 111 111 111 111 111 111 111 111 111 111 111
XX DB 2315 TGATACCTGATTAATGATTAATTTTCGCTGTTCAATTCATGGAATGGGCA 2256
XX
XX QY 104 GGACACACACA 113
XX ID 11111 111
XX DB 2255 GGACATATAAA 2246
XX
XX RESULT 30
XX AAV15422/c
XX ID AAV15422 standard; DNA; 29392 BP.
XX XX
XX AC AAV15422;
XX
XX DT 11-JUN-1998 (first entry)
XX
XX DE Mouse poly Ig receptor protein gene.
XX XX
XX XX Mouse poly Ig receptor protein; pigr protein; pigr deficiency;
XX XX knockout mouse; disease model; ds.
XX OS Mus sp.
XX PN JP10057066-A.
XX PD 03-MAR-1998.
XX
XX PF 19-AUG-1996; 96JP-0217154.
XX PR 19-AUG-1996; 96JP-0217154.
XX XX
XX PA (HONS ) YAKULT HONSHA KK.
XX DR WPI: 1998-254323/23.
XX PT Mouse pig receptor protein gene - used for preparing gene knockout
XX PT mice, useful for study of human poly Ig receptor protein deficiency
XX

```

XX Claim 1: Page 4-14; 18pp; Japanese.
XX
XX
CC The present sequence represents the mouse poly Ig receptor protein
CC gene, which has a 29392 bp sequence. The new gene can be used to
CC produce a gene knockout mouse, useful as a disease model of human
CC poly Ig receptor protein deficiency.
XX
SQ Sequence 29392 BP; 8318 A; 6747 C; 6514 G; 7813 T; 0 other;

Query Match 22.1%; Score 26.8; DB 19; Length 29392;
Best Local Similarity 64.5%; Pred. No. 48;
Matches 40; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 30 GACGCTGCCATGCTGATTAATGAGCGGCTGATTCATTTGCTGTGTTAATGCT 89
DB 21417 GACCTTCTCCACTGCTGGCAGATGACGCCACGATCTTGCGTTAGTGAATATGT 21358
QY 90 TG 91
DB 21357 TG 21356

RESULT 31
AAK78746
ID AAK78746 standard; DNA; 33513 BP.
XX
AC AAK78746;
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33558.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytosolic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
PN WO200157182-A2.
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 23-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0227009.
PR 01-SEP-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237040.
PR 02-OCT-2000; 2000US-0237049.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.

	PR	08-NOV--2000;	2000US-	-0246611.	
	PR	08-NOV--2000;	2000US-	-0246613.	
	PR	17-NOV--2000;	2000US-	-0249207.	
	PR	17-NOV--2000;	2000US-	-0249208.	
	PR	17-NOV--2000;	2000US-	-0249209.	
	PR	17-NOV--2000;	2000US-	-0249210.	
	PR	17-NOV--2000;	2000US-	-0249211.	
	PR	17-NOV--2000;	2000US-	-0249212.	
	PR	17-NOV--2000;	2000US-	-0249213.	
	PR	17-NOV--2000;	2000US-	-0249214.	
	PR	17-NOV--2000;	2000US-	-0249215.	
	PR	17-NOV--2000;	2000US-	-0249216.	
	PR	17-NOV--2000;	2000US-	-0249217.	
	PR	17-NOV--2000;	2000US-	-0249218.	
	PR	17-NOV--2000;	2000US-	-0249244.	
	PR	17-NOV--2000;	2000US-	-0249245.	
	PR	17-NOV--2000;	2000US-	-0249264.	
	PR	17-NOV--2000;	2000US-	-0249265.	
	PR	17-NOV--2000;	2000US-	-0249297.	
	PR	17-NOV--2000;	2000US-	-0249299.	
	PR	17-NOV--2000;	2000US-	-0249300.	
	PR	01-DEC--2000;	2000US-	-0250160.	
	PR	01-DEC--2000;	2000US-	-0250391.	
	PR	05-DEC--2000;	2000US-	-0251030.	
	PR	05-DEC--2000;	2000US-	-0251988.	
	PR	05-DEC--2000;	2000US-	-0256719.	
	PR	06-DEC--2000;	2000US-	-0251479.	
	PR	08-DEC--2000;	2000US-	-0251856.	
	PR	08-DEC--2000;	2000US-	-0251868.	
	PR	08-DEC--2000;	2000US-	-0251869.	
	PR	08-DEC--2000;	2000US-	-0251989.	
	PR	08-DEC--2000;	2000US-	-0251990.	
	PR	11-DEC--2000;	2000US-	-0254097.	
	PR	05-JAN--2001;	2001US-	-0259678.	
XX	(HUMA-) HUMAN GENOME SCI INC.				
PA	Rosen CA,	Barash SC,	Ruben SW;		
XI	WPI:	2001-483426/52.			
DR	Nucleic acids encoding human immune/hematopoietic antigen polypeptides, PT useful for preventing, diagnosing and/or treating cancers and PT metastasis -				
XX	Disclosure; SEQ ID NO 33558; 3071bp + Sequence Listing; English. PS AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) SS amino acid sequences given in AAM82170 to AAM91921. (I) have cytosstatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/hematopoietic-related diseases, especially CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703 CC to AAK87694 represent human Immune/hematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169 CC represent sequences used in the exemplification of the present invention. XX				
SQ	Sequence 33513 BP; 10336 A; 6612 C; 6676 G; 9889 T; 0 other; Query Match 22.1%; Score 26.8; DB 22; Length 33513; Best Local Similarity 59.0%; Pred. No. 51; Matches 46; Conservative 0; Mismatches 32; Indels 0; Gaps 0				
OY	' 33 GCTGCCATCGCATGAATAAGCAGGCGCCGCATGGCAATTGTTCGTTGTAATAAATTTTGT 92 "				

```

Db 11667 GCCTCTAAACGCTGGAAATTACAGTCTGTAGACCACTGTGCTGTCTCAATAAACCTTTT 11726
QY 93 ATAATTGAGCAGGACACA 110
      | | | | | | | |
Db 11727 AAATTCCATCCACATTACA 11744

RESULT 32
AA081965
ID AA081965 standard; DNA; 294 BP.
XX
AC AA081965;
XX
DT 17-DEC-2001 (updated)
DT 08-OCT-1990 (first entry)
XX
DE Clone Am4 encoding brain amyloid of Alzheimer's disease and adult
DE Down's syndrome.
XX
KW Clone Am4; beta amyloid; Alzheimer's disease; adult Down's syndrome; ss
XX
PN USN7019001-N.
XX
PD 27-OCT-1987.
XX
PE 26-FEB-1987; 87US-0091001.
XX
PR 26-FEB-1987; 87US-0091001.
XX
PA (USSH ) US DEPT HEALTH AND HUMAN.
XX
DR WPI: 1988-021389/03.
XX
P-PSDB; P981517.
XX
PT cdna clone encoding amyloid polypeptide of Alzheimer's disease
PT obtd. from adult human brain cdna library using oligonucleotide
PT probe.
XX
PS Disclosure: ; P: English.
XX
CC The clone encodes the beta amyloid protein found in Alzheimer's disease.
CC It can be used to study neuropathological changes in Alzheimer's, adult
CC Down's syndrome, Guamian amyotrophic lateral sclerosis/Parkinsonism-
CC dementia and the ageing brain.
CC (Note: Revised entry submitted to correct the patent number format of
CC US Government-owned NRTS applications to prevent clashes with ongoing US
CC granted patent numbers. For further information visit the Derwent
CC web site at www.derwent.com/dwpl/updates/ntls-us.html.)
XX
SQ Sequence 294 BP; 85 A; 63 C; 77 G; 69 T; 0 other:

Query Match 22.0%; Score 26.6; DB 9; Length 294;
Best Local Similarity 58.0%; Pred. No. 11;
Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps

QY 11 TAGCTCGGTGGAGACAGATCGACGCTGCCCATGCTGATAAATGACGAGGCTCTGATTCATTG 70
      ||| ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| |||||
Db 116 TAGGACAGCATGATGTCATCACTGCTGTGATGCTGAAGAAACAAACATACATTCATTTC 175
      ||| ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| |||||

QY 71 TTGCTGTGTTATTAATGTTG 91
      ||| ||||| ||| ||| ||||| ||| ||| |||||
Db 176 ATCATGCTGTGCTGGAGGTTG 196

RESULT 33
AA088696
ID AA088696 standard; cDNA to mRNA; 297 BP.
XX
AC AA088696;
XX
DT 11-NOV-1995 (first entry)
XX
DE Beta-amyloid precursor protein C-terminal peptide gene.

```

```

XX  Human; beta-amyloid precursor protein; C-terminal peptide;
KW  gene transfer; transgenic animal; Alzheimer disease model;
XX  gene therapy; ss.
XX  Homo sapiens.
XX  EP653154-A.
XX  17-MAY-1995.
XX  07-NOV-1994; 94EP-0117512.
XX  12-NOV-1993; 93JP-0306026.
XX  (FARH ) HOECHST JAPAN LTD.
PA  (FARH ) HOECHST JAPAN KK.
XX  Kowabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
PI  WPI: 1995-180492/24.
DR  P-PSDB: AAR74694.
XX  Transgenic animal model for Alzheimer's disease - contains DNA encoding
PT  part of beta-amyloid precursor protein in a gene construct designed for
XX  over-expression in various cell types
XX  Claim 2; Page 11; 32pp; English.
XX  The sequence encodes a human brain beta-amyloid precursor protein
CC  (APP) C-terminal peptide. The DNA may be transferred along with an
CC  APP signal peptide gene (e.g. AA088695) into somatic and germ cells of
CC  a non-human mammal, and the resulting transgenic animal may be used
CC  as a model for Alzheimer disease (AD). The animal model exhibits
CC  symptoms similar to AD, producing large quantities of APP C-terminal
CC  peptide, death of neuron cells in pyramidal cells at cerebral
CC  amyloid regions, increases in glial cells and deposition of
CC  abnormally phosphorylated tau protein. The animal model may be
CC  used to develop new therapies for AD, including gene therapy
XX  strategies.
XX  Sequence 297 BP; 86 A; 64 C; 78 G; 69 T; 0 other;
SQ
XX  Query Match 22.0%; Score 26.6; DB 16; Length 297;
XX  Best Local Similarity 58.0%; Pred. No. 12;
XX  Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
XX  QY 11 TAGCCTGGTGGACAGATCGACGCTGCCCATCGATTAATGAGCGTCCATGCATTG 70
XX  DB 122 TAGCGACAGTATGCTCATCTGATGCTGAAGAGAAACAGTACACATCCATTG 181
XX  QY 71 TTGGTTGTATTAAATGTTG 91
XX  DB 182 ATCATGCTGTGTGGAGGTTG 202
XX  RESULT 34
XX  AA088697
XX  ID AA088697 standard; cDNA to mRNA; 297 BP.
XX  AC AA088697;
XX  DT 11-NOV-1995 (first entry)
XX  DE Beta-amyloid precursor protein C-terminal peptide mutant gene.
XX  KW Human; beta-amyloid precursor protein mutant; C-terminal peptide;
XX  KW gene transfer; transgenic animal; Alzheimer disease model;
XX  KW gene therapy; ss.
XX  OS Homo sapiens.
XX  EP653154-A.

```

```

XX  17-MAY-1995.
XX  07-NOV-1994; 94EP-0117512.
XX  12-NOV-1993; 93JP-0306026.
XX  (FARH ) HOECHST JAPAN LTD.
PA  (FARH ) HOECHST JAPAN KK.
XX  Kowabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
PI  WPI: 1995-180492/24.
DR  P-PSDB: AAR74695.
XX  Transgenic animal model for Alzheimer's disease - contains DNA encoding
PT  part of beta-amyloid precursor protein in a gene construct designed for
XX  over-expression in various cell types
XX  Claim 2; Page 12-13; 32pp; English.
XX  The sequence encodes a human brain beta-amyloid precursor protein
CC  (APP) mutant C-terminal peptide, and differs from AA088696 by a Glu
CC  to Gln conversion at codon 22. The DNA may be transferred along
CC  with an APP signal peptide gene (e.g. AA088695) into somatic and germ
CC  cells of a non-human mammal, and the resulting transgenic animal may
CC  be used as a model for Alzheimer disease (AD). The animal model
CC  exhibits symptoms similar to AD, producing large quantities of APP
CC  C-terminal peptide, death of neuron cells in pyramidal cells at
CC  cerebral amyloid regions, increases in glial cells and deposition
CC  of abnormally phosphorylated tau protein. The animal model may
CC  be used to develop new therapies for AD, including gene therapy
XX  strategies.
XX  Sequence 297 BP; 86 A; 65 C; 77 G; 69 T; 0 other;
SQ
XX  Query Match 22.0%; Score 26.6; DB 16; Length 297;
XX  Best Local Similarity 58.0%; Pred. No. 12;
XX  Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
XX  QY 11 TAGCCTGGTGGACAGATCGACGCTGCCCATCGATTAATGAGCGTCCATGCATTG 70
XX  DB 122 TAGCGACAGTATGCTCATCTGATGCTGAAGAGAAACAGTACACATCCATTG 181
XX  QY 71 TTGGTTGTATTAAATGTTG 91
XX  DB 182 ATCATGCTGTGTGGAGGTTG 202
XX  RESULT 35
XX  AA042665
XX  ID AA042665 standard; cDNA; 300 BP.
XX  AC AA042665;
XX  DT 27-OCT-1993 (first entry)
XX  DE Full-length beta-amyloid protein coding region.
XX  KW Alzheimer's Disease; Amyloid Plaque Core Protein; APCP;
XX  KW neuritic plaque; ds.
XX  OS Homo sapiens.
XX  FH Key location/Qualifiers
XX  CDS 1..300
XX  FT /*tag= a
XX  FT /product= beta-amyloid-protein
XX  FT /note= "full-length coding sequence obtained by
XX  FT combining overlapping clones SM2W3 and
XX  FT SM2W4 (AA042664 and AA042663, respectively)"
XX  FT misc_difference 160..162
XX  FT /*tag= b

```

FT	/codon= seq: AAC; aa: Lys
FF	/note= "this codon is AAG in AAQ42664"
XX	
FN	US5220013-A.
PD	15-JUN-1993.
XX	
PF	17-NOV-1986;
XX	86US-0932193.
PR	17-NOV-1986;
PR	31-DEC-1986;
PR	30-JAN-1987;
PR	18-AUG-1987;
PR	30-NOV-1989;
XX	86US-00948376.
XX	87US-0008810.
XX	87US-0087002.
PA	(SCIO-) SCIOS NOVA INC.
PI	Cordell B, Ponte PA.
DR	WPI; 1993-205383/25.
DR	P-PSDB; AAR37866.
XX	
PT	DNA sequence useful for detection of Alzheimer's disease - for
PT	encoding beta amyloid core protein
XX	
PS	Disclosure; Fig 5; 40pp; English.
XX	
CC	A clone was obtained from the genomic library described in Lawn et al.,
CC	Cell, 15:1157-1174 (1978) which included a 57 base pair segment which
CC	encodes amino acids 1-18 of the beta-amyloid protein, immediately
CC	preceded by a Methionine. A HindIII/SalI fragment derived from the
CC	genomic clone and containing the 57bp segment was used to isolate cDNA
CC	fragments from a library prepared from temporal and parietal cortical
CC	tissue from a normal human brain. Lambda clone SM2W3 (AAQ42664) contains
CC	a 5' region segment which has a 6bp overlap with the 3' end of clone
CC	SM2W4 (AAQ42663). The full-length beta-amyloid protein coding sequence
CC	(AAQ42665), including an initiator Met residue which is probably
CC	processed in vivo, was obtained by combining the sequences of the
CC	two overlapping clones.
XX	
SQ	Sequence 300 BP; 87 A; 65 C; 78 G; 70 T; 0 other;
XX	
Query Match	22.0%; Score 26.6; DB 14; Length 300;
Best Local Similarity	58.0%; Pred. No. 12;
Matches 47; Conservative	0; Mismatches 34; Indels 0; Gaps 0;
OY	11 TAGCCTCGGTGACAGATCGACGCTGCCCATGATAAATGACGGTCCGATTCATTG 70
Db	
125	TAGCAGCAGTAGTGCTGCATCACTCGTTGGATGCTGAACAAGAAGTACACATCATTC 184
OY	71 TTTCGTTGTTTAATTAAATGTTG 91
Db	
185	ATCATGTGTGTGTGGAGGTTG 205
RESULT 36	
AAK93386	
ID	AAK93386 standard; DNA: 300 BP.
XX	
AC	AAK93386;
XX	
DT	27-JUN-2002 (first entry)
XX	
DE	DNA of wild type C99 portion of human APP.
XX	
KM	Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;
KM	Amyloid precursor protein; tissue-specific expression control; human APP;
KM	APP pathway modulator; gene therapy; ds.
XX	
OS	Homo sapiens.
XX	
XX	'WO200226820-A2.
XX	

[illegible]

PR 24-OCT-1998; 98DE-1049073.
XX (AVET) AVENTIS PHARMA DEUT GMBH.
XX
XX
XX Peraus G, Hoppe E, Baumeister R;
XX WPI; 2000-304753/27.
XX
XX Transgene encoding amyloid precursor protein or its fragment, used to
PT produce transgenic nematodes used, e.g. to screen for agents for
PT treating Alzheimer's disease
XX
XX
XX Claim 3; Page 6; 16pp; German.
XX
XX This invention describes a novel transgene (I) which comprises (i) a
CC sequence (Ia) that encodes either the complete amyloid precursor protein
CC (APP) or a part of its Abeta peptide (Abp), but is not identical with
CC the part of the APP sequence that encodes the complete Abp; (ii)
CC optionally one or more additional coding and/or non-coding sequences and
CC (iii) a promoter functional in *Caenorhabditis elegans*. Cleavage of APP
CC by alpha-secretase does not lead to Abp, but cleavage with beta or
CC gamma-secretase does, so modulation of these activities is used to
CC reduce the amount of APP, a major component of the plaque found in
CC Alzheimer patients, produced. (I), or expression vectors containing it,
CC are used to produce transgenic cells (optionally part of a non-human
CC animal), specifically *C. elegans*. The transgenic animals are used (i) to
CC identify gamma and/or alpha-secretase activities in *C. elegans*; (ii) to
CC identify/or characterize substances that inhibit gamma-secretase or
CC increase alpha-secretase activities, or (iii) to identify and/or
CC characterize agents potentially useful for treatment or prevention of
CC Alzheimer's disease. This sequence represents the human APP protein C100
CC fragment which is used in the construction of the transgene described in
CC the method of the invention.
XX
XX Sequence 303 BP; 87 A; 65 C; 80 G; 71 T; 0 other;
SQ
Query Match 22.0%; Score 26.6; DB 21; Length 303;
Best Local Similarity 58.0%; Pred. No. 12;
Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
OY 11 TAGCCTCGGTGACAGATCGACGCTGCCATCGTATTAATGAGCGTCCATCATTTG 70
DB 125 TAGCGACAGTATGCTCATCTGATCGTGATGCTGAAGAAGAACAGTACACATCATTC 184
OY 71 TTCGTTGTGTTATTAATGTTG 91
DB 185 ATCATGCTGTGCTGAGAGTTG 205
RESULT 38
AA088699
ID AA088699 standard; cDNA to mRNA; 309 BP.
XX
XX AA088699;
XX
XX 11-NOV-1995 (first entry)
XX
XX Beta-amyloid precursor protein C-terminal peptide gene.
XX
XX Human; beta-amyloid precursor protein; C-terminal peptide;
KW gene transfer; transgenic animal; Alzheimer disease model;
XX gene therapy; ss.
XX
XX Homo sapiens.
XX
XX EP653154-A.
XX
XX 17-MAY-1995.
XX
XX 07-NOV-1994; 94EP-0117512.
XX
XX 12-NOV-1993; 93JP-0306026.
XX

PA (FARH) HOECHST JAPAN LTD.
PA (FARH) HOECHST JAPAN KK.
XX
XX Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
XX WPI; 1995-180492/24.
XX
XX P-PSDB; AAR74697.
XX
XX Transgenic animal model for Alzheimer's disease - contains DNA encoding
PT part of beta-amyloid precursor protein in a gene construct designed for
PT over-expression in various cell types
XX
XX
XX Claim 2; Page 15; 32pp; English.
XX
XX The sequence encodes a human brain beta-amyloid precursor protein
CC (APP) C-terminal peptide. The DNA may be transferred along with an
CC APP signal peptide gene (e.g. AA088695) into somatic and germ cells
CC of a non-human mammal, and the resulting transgenic animal may be
CC used as a model for Alzheimer disease (AD). The animal model
CC exhibits symptoms similar to AD, producing large quantities of APP
CC C-terminal peptide, death of neuron cells in pyramidal cells at
CC cerebral amyloid regions, increases in glial cells and deposition
CC of abnormally phosphorylated tau protein. The animal model may
CC be used to develop new therapies for AD, including gene therapy
CC strategies.
XX
XX Sequence 309 BP; 91 A; 64 C; 83 G; 71 T; 0 other;
SQ
Query Match 22.0%; Score 26.6; DB 16; Length 309;
Best Local Similarity 58.0%; Pred. No. 12;
Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
OY 11 TAGCCTCGGTGACAGATCGACGCTGCCATCGTATTAATGAGCGTCCATCATTTG 70
DB 134 TAGCGACAGTATGCTCATCTGATCGTGATGCTGAAGAAGAACAGTACACATCATTC 193
OY 71 TTCGTTGTGTTATTAATGTTG 91
DB 194 ATCATGCTGTGCTGAGAGTTG 214
RESULT 39
AA088700
ID AA088700 standard; cDNA to mRNA; 309 BP.
XX
XX AA088700;
XX
XX 11-NOV-1995 (first entry)
XX
XX Beta-amyloid precursor protein C-terminal peptide mutant gene.
XX
XX Human; beta-amyloid precursor protein mutant; C-terminal peptide;
KW gene transfer; transgenic animal; Alzheimer disease model;
XX gene therapy; ss.
XX
XX Homo sapiens.
XX
XX EP653154-A.
XX
XX 17-MAY-1995.
XX
XX 07-NOV-1994; 94EP-0117512.
XX
XX 12-NOV-1993; 93JP-0306026.
XX
XX (FARH) HOECHST JAPAN LTD.
XX (FARH) HOECHST JAPAN KK.
XX
XX Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
XX WPI; 1995-180492/24.
XX P-PSDB; AAR74698.
XX

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding
 PT part of beta-amyloid precursor protein in a gene construct designed for
 PT over-expression in various cell types
 XX
 PS Claim 2: Page 16-17; 32pp; English.
 CC The sequence encodes a human brain beta-amyloid precursor protein
 CC (APP) mutant C-terminal peptide, and differs from AA088699 by
 CC conversion of Lys to Asn at codon-3 and Met to Leu at codon-4. The
 CC DNA may be transferred along with an APP signal peptide gene (e.g.
 CC AA088699) into somatic and germ cells of a non-human mammal, and the
 CC resulting transgenic animal may be used as a model for Alzheimer
 CC disease (AD). The animal model exhibits symptoms similar to AD,
 CC producing large quantities of APP C-terminal peptide, death of
 CC neuron cells in pyramidal cells at cerebral amyloid regions,
 CC increases in glial cells and deposition of abnormally
 CC phosphorylated tau protein. The animal model may be used to develop
 CC new therapies for AD, including gene therapy strategies.
 CC
 SQ Sequence 309 BP; 90 A; 65 C; 82 G; 72 T; 0 other;
 Query Match 22.0%; Score 26.6; DB 16; Length 309;
 Best Local Similarity 58.0%; Pred. No. 12;
 Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 11 TAGCCTCGGTGACAGATCGACGCTGCCCTGATTAATGAGCGCTCTGATCCATTG 70
 DB 134 TAGCGAGAGTGCATCGTCATCCTGTGATGCTGAAGAAGACATACATCATTC 193
 OY 71 TTGCTGTGTATTATGTTG 91
 DB 194 ATCATGCTGTGTCGAGGTTG 214
 RESULT 40
 AAD20982
 ID AAD20982 standard; DNA; 315 BP.
 AC AAD20982;
 XX
 DT 15-JAN-2002 (first entry)
 XX
 DE Human recombinant beta-amyloid precursor protein (betaAPP) C-83 DNA.
 XX
 KW Human; Alzheimer's disease; gamma-secretase; integral-membrane protein;
 KW beta-amyloid precursor protein; betaAPP; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..315
 FT /tag= a
 FT /product= "Human recombinant betaAPP protein (C-83)"
 PN WO200175435-A2.
 XX
 PD 11-OCT-2001.
 XX
 PE 30-MAR-2001; 2001WO-US10453.
 XX
 PR 03-APR-2000; 2000US-194495P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Roberts SB, Hendrick JP, Vintsky A, Lewis M, Smith DW, Pak R;
 XX
 DR WPI: 2001-648575/74.
 DR P-PSDB: AAE12897.
 XX
 PT Novel gamma secretase protein, useful in the production of amyloids, is
 PT capable of cleaving beta-amyloid precursor protein to produce beta
 PT amyloid peptide
 XX

PS Example 1: Fig 3; 127pp; English.
 XX
 CC The invention relates to the field of plaque amyloid deposits that are
 CC the hallmarks of Alzheimer's disease. In particular, the invention
 CC relates to an isolated, functionally-active protein that has
 CC gamma-secretase activity. Gamma-secretase activity is necessary for
 CC amyloid production. The present invention also relates to methods for
 CC isolating integral-membrane proteins and protein complexes, including
 CC the gamma-secretase protein of the invention. The method is useful for
 CC monitoring the cleavage of beta-amyloid precursor protein (betaAPP)
 CC by gamma-secretase. The present sequence is a DNA encoding human
 CC recombinant betaAPP protein (C-83).
 CC
 SQ Sequence 315 BP; 75 A; 75 C; 92 G; 73 T; 0 other;
 Query Match 22.0%; Score 26.6; DB 22; Length 315;
 Best Local Similarity 58.0%; Pred. No. 12;
 Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 11 TAGCCTCGGTGACAGATCGACGCTGCCCTGATTAATGAGCGCTCTGATCCATTG 70
 DB 137 TAGCGAGAGTGCATCGTCATCCTGTGATGCTGAAGAAGACATACATCATTC 196
 OY 71 TTGCTGTGTATTATGTTG 91
 DB 197 ATCATGCTGTGTCGAGGTTG 217
 RESULT 41
 AAD23935
 ID AAD23935 standard; DNA; 327 BP.
 AC AAD23935;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Gamma-secretase substrate #1 DNA.
 XX
 KW Gamma-secretase substrate; beta-CTF domain; amyloid precursor protein;
 KW APP; beta-secretase; Alzheimer's disease; fusion protein; ds.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..327
 FT /tag= a
 FT /product= "Gamma-secretase substrate"
 FT /note= "This substrate contains APP beta-CTF domain and
 FT hydrophilic moiety fusion"
 FT misc-feature 1..300
 FT /tag= b
 FT /note= "APP beta-CTF domain DNA"
 FT misc-feature 301..324
 FT /tag= c
 FT /note= "Region encoding hydrophilic moiety"
 PN WO200183811-A1.
 XX
 PD 08-NOV-2001.
 XX
 PE 25-APR-2001; 2001WO-US13332.
 XX
 PR 01-MAY-2000; 2000US-201053P.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Li Y, Xu M, Huang Q, Gardell S;
 XX
 DR WPI: 2002-066536/09.
 DR P-PSDB: AAE14379.
 XX
 PT Novel gamma secretase substrate for assaying gamma secretase activity
 PT and identifying compounds that regulate gamma secretase activity, e.g.
 PT

PT Inhibitors of gamma secretase useful for treating Alzheimer's disease
 XX
 XX
 PS Example 1; Page 12-13; 36pp; English.
 XX
 CC The invention relates to gamma-secretase substrates containing
 CC a hydrophilic polypeptide moiety covalently joined to the carboxyl
 CC terminus of a beta-CTF domain. A beta-CTF domain is a polypeptide that
 CC can be cleaved by gamma-secretase, and that approximates the
 CC C-terminal fragment (amino acids 596-695) of amyloid precursor protein
 CC (APP) produced after cleavage of APP by beta-secretase. The
 CC hydrophilic polypeptide moiety increases the solubility of the
 CC substrate in a zwitterionic detergent. The gamma-secretase substrate
 CC is used in vitro assays employing zwitterionic detergent for
 CC measuring gamma-secretase activity. The assay methods are useful for
 CC purifying and characterizing the enzyme, to screen for compounds that
 CC modulate gamma-secretase activity, and to test the ability of a
 CC particular compound that affect gamma-secretase activity. The compounds
 CC that modulate gamma-secretase activity include gamma-secretase
 CC inhibitors which are useful in the treatment of Alzheimer's disease,
 CC and in the characterisation of the biological importance of
 CC gamma-secretase. The present sequence is a DNA encoding gamma-secretase
 CC substrate of the invention. The substrate is a fusion protein
 CC containing APP beta-CTF domain and a hydrophilic moiety.
 XX
 SO Sequence 327 BP; 100 A; 68 C; 85 G; 74 T; 0 other;
 Query Match 22.0%; Score 26.6; DB 24; Length 327;
 Best Local Similarity 58.0%; Pred. No. 12;
 Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 OY 11 TAGCCTCGGTGACAGATCGCTGCCATCTGATTAATGACGCTCTGATTCATTG 70
 DB 125 TAGCAGACAGTATCTCATACCTTGATGATCTGTAGAGAAGAACAGTACATCATTC 184
 OY 71 TTCGTTGCTTATTAATGTTG 91
 DB 185 ATCATGCTGTGCTGGAGTTG 205
 DB 10-OCT-1996 (first entry)
 XX
 DE Familial Alzheimer's disease APP isoform 751 gene fragment.
 XX
 KW APP; amyloid precursor protein; isoform 751; inherent; familial;
 KW Alzheimer's disease; mutation; diagnosis; transgenic model; study;
 KW cognitive; beta A4 domain; exon 17; senility; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Exon 1..336
 FT /tag= a
 FT /number= 17
 FT /transl_except= pos: 175-177, aa: Ile
 FT /note= "encodes amino acids 640-751 of full APP
 FT isoform 751, the translation exception
 FT at posn. 175-177 is the site of a Val to
 FT Ile mutation in isoform 751, bases 175-177
 FT probably should be ATC and not TTC"
 FT misc_feature 43..168
 FT /tag= b
 FT /note= "encodes the beta-A4 domain"
 XX
 PN WO9606927-A1.
 XX
 PD 07-MAR-1996.

XX
 PF 28-AUG-1995; 95WO-US10920.
 XX
 PR 01-SEP-1994; 94US-0299872.
 XX
 XX (MERI) MERCK & CO INC.
 PA
 PI Chen HY, Heavens RP, Singh G, Srinathsinghji DJS;
 PI Smith DW, Trumbauer ME, Van Der Ploeg LHT, Vongs A;
 PI Zheng H;
 XX
 DR WPI; 1996-160358/16.
 DR P-PSDB; AAR93556.
 XX
 PT Transgenic animal expressing familial form of human amyloid
 PT precursor protein used to evaluate compounds affecting
 PT Alzheimer's disease and other cognitive disorders
 PS Example 1; Fig 7; 32pp; English.
 XX
 CC AAT18082 represents exon 17 of the amyloid precursor protein (APP)
 CC isoform 751 gene from a patient diagnosed with familial Alzheimer's
 CC disease (FAD). The sequence given corresponds to the coding sequence
 CC for amino acids 640-751 of FAD APP 751. A feature of FAD is a Val to
 CC Ile substitution at posn. 698 of the full APP (encoded by bases 175
 CC to 177 of this sequence). DNA encoding this sequence was used to
 CC construct expression vectors for the prodn. of transgenic animals (esp.
 CC mice) carrying the FAD APP 751 mutation. The transgenic animals are
 CC useful for the evaluation of test cpts. affecting Alzheimer's disease
 CC and other cognitive disorders and for identification of new targets
 CC in Alzheimer's disease since the progression of the disease can be
 CC followed gradually.
 CC N.B. the V-I mutation encoded at base 175-177 is given in the
 CC specification as a TTC codon (most probably this should be ATC).
 XX
 SO Sequence 336 BP; 102 A; 69 C; 88 G; 77 T; 0 other;
 Query Match 22.0%; Score 26.6; DB 17; Length 336;
 Best Local Similarity 58.0%; Pred. No. 12;
 Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 OY 11 TAGCCTCGGTGACAGATCGCTGCCATCTGATTAATGACGCTCTGATTCATTG 70
 DB 161 TAGCGACAGTATCTCATACCTTGATGATCTGTAGAGAAGAACAGTACATCATTC 220
 OY 71 TTCGTTGCTTATTAATGTTG 91
 DB 221 ATCATGCTGTGCTGGAGTTG 241
 DB 16-MAR-1994 (first entry)
 XX
 DE Human brain Expressed Sequence Tag EST00434.
 XX
 KW Gene transcription product; genetic markers; tagging; in vivo;
 KW transcription; mapping; locations; chromosomes; chromosomal; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9316178-A.
 PN 19-AUG-1993.
 PD 12-FEB-1993; 93WO-US01294.
 XX
 PR 12-FEB-1992; 92US-0837195.
 XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
 XX
 PI Adams MD, Moreno RF, Venter CJ.
 XX
 DR WPI: 1993-272882/34.
 XX
 PT Enriched oligonucleotides and corresp. sequences - used as
 PT markers for human genes transcribed in-vivo, facilitate tagging
 PT of most human genes
 XX
 PS Example 4; Page 171; 500pp; English.
 XX
 CC The Expressed Sequence Tag was isolated from a human brain cDNA
 CC library as part of a large set of ESTs which can be used as markers
 CC for human genes transcribed in vivo. They can be used to facilitate
 CC tagging of most human genes, for mapping locations of expressed genes
 CC on chromosomes, for individual or forensic identification, for mapping
 CC locations of disease-associated genes, for identification of tissue
 CC type, and for prep. of antisense sequences, probes and constructs.
 CC EST00434 has a "poor" coding probability as evaluated using the
 CC coding-region prediction program CRM. See also AAO59041-Q61440.
 CC
 SQ Sequence 337 BP; 95 A; 63 C; 66 G; 107 T; 6 other;
 XX
 Query Match 22.0%; Score 26.6; DB 14; Length 337;
 Best Local Similarity 54.9%; Pred. No. 12;
 Matches 50; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
 OY 11 TAGCCTCGGTGACAGATCGATGCCATGCTGATAAATGAGCGCTCCTGATCCATTG 70
 DB 58 TTAGCTTAGCGCTTCTGAGATCACTTCCCTCTTATAAATGAGAGAAATATCCATTG 117
 OY 71 TTGCTGTGTATTATTAATGTTGATATGAG 101
 DB 118 CTCATTGAGTTGTTAATNAGACATAAATGAG 148
 XX
 RESULT 44
 AAV07188
 ID AAV07188 standard; DNA: 354 BP.
 XX
 AC AAV07188;
 XX
 DT 09-SEP-1998 (first entry)
 XX
 DE Flag-amyloid protein precursor (FLAG-APP-C100) fusion protein.
 XX
 KW Amyloid protein precursor; APP-C100; fusion protein; FLAG-APP-C100;
 KW transgenic animal; Alzheimer's disease; mouse; neurodegeneration;
 KW brain; ss.
 XX
 OS Chimeric - Synthetic.
 OS Chimeric - Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..351
 FT /tag= a
 FT /product= "FLAG-APP-C100"
 FT /note= "no start or stop codon specified"
 XX
 PN W09816627-A1.
 XX
 PD 23-APR-1998.
 XX
 PF 16-OCT-1997; 97WO-US18202.
 XX
 PR 16-OCT-1996; 96US-0729345.
 XX
 PA (MCLE-) MCLEAN HOSPITAL CORP.
 PA (WELL-) WELLESLEY COLLEGE.
 XX
 PI Berger-Sweeney J, Neve RL;
 XX

DR WPI: 1998-251279/22.
 DR P-PSDB: AAW51102.
 XX
 PT Transgenic animal with rapid development of Alzheimer disease
 PT characteristics - contains nucleic acid encoding fragment of amyloid
 PT protein precursor fused to flag peptide, useful as model for
 PT screening potential therapeutic agents
 XX
 PS Claim 5; Pages 26-27; 41pp; English.
 XX
 CC This is the nucleotide sequence of the FLAG-Amyloid protein precursor
 CC (FLAG-APP-C100), used in the method of the invention, involving the
 CC creation of an FLAG-amyloid protein precursor fusion protein, as well
 CC as a transgenic animal with rapid development of Alzheimer's disease.
 CC The animals, specifically mice, show increased neurodegeneration in the
 CC brain and cognitive impairment, so are used as in vivo models for
 CC screening agents potentially useful in treatment of Alzheimer's disease.
 XX
 SQ Sequence 354 BP; 107 A; 71 C; 95 G; 81 T; 0 other;
 XX
 Query Match 22.0%; Score 26.6; DB 19; Length 354;
 Best Local Similarity 58.0%; Pred. No. 12;
 Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 OY 11 TAGCCTCGGTGACAGATCGATGCCATGCTGATAAATGAGCGCTCCTGATCCATTG 70
 DB 176 TAGCGACAGTGTGTCATCACTTGATGTCGTAAGAAAGACATACATCCATTG 235
 OY 71 TTGCTGTGTATTATTAATGTTG 91
 DB 236 ATCATGTGTGTGCTGAGAGTTG 256
 XX
 RESULT 45
 AAV20379
 ID AAV20379 standard; DNA: 354 BP.
 XX
 AC AAV20379;
 XX
 DT 26-JUN-1998 (first entry)
 XX
 DE DNA for APP C-terminal fragment mutant SPACT Thr43pne.
 XX
 KW Human; amyloid precursor protein; APP; carboxy-terminal fragment;
 KW A4CT; mutant SPACT Thr43pne; disease model; treatment;
 KW Alzheimer's disease; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..354
 FT /tag= a
 FT /note= "stop codon not given"
 XX
 PN W09803643-A2.
 XX
 PD 29-JAN-1998.
 XX
 PF 17-JUL-1997; 97WO-EP03960.
 XX
 PR 08-MAY-1997; 97GB-0009239.
 PR 22-JUL-1996; 96GB-0015351.
 PR 09-SEP-1996; 96GB-0018804.
 XX
 PA (SMIK) SMITHKLINE BEECHAM AUSTRALIA PTY LTD.
 PA (SMIK) SMITHKLINE BEECHAM PHARMA GMBH.
 XX
 PI Beyreuther K, Lichtenhaer S, Masters CL, Prior P;
 XX
 DR WPI: 1998-120768/11.
 DR P-PSDB: AAW50029.
 XX

PT Construct containing sequence for mutant form of amyloid precursor protein - or its C-terminal fragment, and related transgenic animals
PT or transformed cells, used for identifying potential drugs for Alzheimer's disease

PS Claim 10; Page 10; 15pp; English.

CC The present sequence encodes the human amyloid precursor protein
CC (APP) C-terminal fragment (A β C7) mutant SPAC7 Thr43Phe.
CC The mutation results in a higher ratio of beta A4 1-42 to beta A4
CC 1-40, useful in disease models to identify potential drugs for the
CC treatment of Alzheimer's disease.

50 Sequence 354 BP; 89 A; 83 C; 99 G; 83 T; 0 other;

Query Match	22.08;	Score 26.6;	DB 19;	Length 354;
-------------	--------	-------------	--------	-------------

Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 11 TAGCTCGGTGGACAGATCGACGCTGCCCATGCTGATTAATGACGGTCTTGATCCATTG 70
 |||| | ||| | ||| ||||| || ||| || |||||
 Db 179 TAGCATTCGATCGTCATCACTTGCTGATGCTGAAGAGAAGACAGTACACATCCATTTC 238

71 TTCGTTGTGTTATTATGTTG 91

Db 239 ATCATGCTGCTGCTGAGGTTG 259

Search completed: April 23, 2003, 15:02:20
Job time : 127.069 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 23, 2003, 12:06:28 ; Search time 10.0833 seconds
(without alignments)
2307.226 Million cell updates/sec

Title: US-09-198-779B-1_COPY_1_121

```

Perfect score: 215
Sequence:      1 gtttcgctctagcctcgt.....caggaacacacacgtacgt 121

```

Scoring table:			
	BLOSUM62		
Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

```
Searched:      283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 566448
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 50 summaries

```

```

Command line parameters:
-MODEL=framed+.n2p.model -DEV=xip
-o/cgn2.1.uspnt.spool/US09198779/r/unat.23042003-1.120617-2416/app_query.fasta.1.9177
-DB=trir.73 -USPNT=fastlan -SUFFIX=run -MINMATCH=0.1 -LOEPC1=0 -LOEPC2=0 -LOEPC3=0
-UNITS=bits -START=1 -END=1 -MATRIX=blotsum62 -TRANS=human40.cdi -LIST=50
-DOCLG1Gn=200 -THR.SCORE=pcpt -THR.MAX=100 -THR.MIN=0 -ALIAS=45 -MODE=LOCAL
-OUTER=pcpt -NORM=ext -HAPSITE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09198779 -GCN=1.1.92 -ETUNE=23042003-1.120617-2416 -NCPU=6
-NO.XLXPT -NO.MMAP -LARGEOBJECT -NES.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXP=0.5 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```

```
Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	length	ID	Description
No.	Score				
1	61	28.4	877	2 AC2211	heme transport pro
2	58.5	27.1	155	2 H89787	hypothetical prote
3	58	27.0	472	2 G75298	ribosomal protein
4	56	25.9	701	2 T17243	hypothetical prote
5	55	25.5	86	2 T31059	hypothetical prote
6	55	25.6	365	2 T29224	hypothetical prote
7	35	25.6	881	1 KGBT64	regulatory protein
8	54.5	25.2	2110	2 B44110	mycocerotate synth
9	54.5	25.2	2111	2 A70658	mycocerotate synth
10	54.5	25.2	2116	2 C86926	probable mycoceros
11	54	25.0	382	1 S2652	transcription fact
12	54	25.1	616	2 T08708	hypothetical prote
13	54	25.0	737	2 T15587	hypothetical prote
14	54	25.0	849	2 T22306	hypothetical prote

C 15	-	54	25.0	1017	2	T15598	hypothetical prote
C 16	53.5	124.8	1174	2	T49868	related to suppress	
C 17	53	24.7	134	2	A87423	hypothetical protee	
C 18	53	24.5	302	2	F90445	conserved hypothet	
C 19	53	24.7	400	2	B69081	acetyl-CoA synthet	
C 20	53	24.5	928	2	T24868	hypothetical protee	
C 21	53	24.5	1844	2	D71612	hypothetical prote	
C 22	53	24.5	2715	2	T13049	hypothetical prote	
C 23	52	24.1	388	2	G95375	eyelid - fruit fly	
C 24	52	24.2	451	2	G63916	probable drug resi	
C 25	52	24.1	763	2	C51598	glycolate oxidase	
C 26	52	24.2	1091	2	C75585	gene COX1 intcon 4	
C 27	51.5	23.8	627	2	S48424	carboxylase - Dein	
C 28	51.5	23.8	1469	2	T24216	hypothetical prote	
C 29	51.5	23.8	2126	2	E70522	chromosome condens	
C 30	51	23.7	371	2	T04971	probable polyketid	
C 31	51	23.7	399	2	T47873	hypothetical prote	
C 32	51	23.7	433	2	T32605	phosphatidate cyti	
C 33	51	23.6	559	1	J02010	hypothetical prote	
C 34	51	23.7	884	2	T18649	transcription fact	
C 35	51	23.6	885	2	T18698	hypothetical prote	
C 36	51	23.6	922	2	F81539	100 kDa coactivato	
C 37	51	23.6	922	2	B72131	polymorphic membra	
C 38	51	23.6	922	2	B72131	polymorphic outer	
C 39	51	23.6	922	2	E86491	polymorphic outer	
C 40	50.5	23.6	1672	2	T46237	hypothetical prote	
C 41	50.5	23.4	179	2	T18144	hypothetical prote	
C 42	50.5	23.5	179	2	AD1012	conserved hypothet	
C 43	50.5	23.4	259	2	T49596	related to H ⁺ -trans	
C 44	50.5	23.4	350	2	B97980	dihydroorotate oxi	
C 45	50.5	23.4	415	2	S39535	corlicotriopin-rele	
C 46	50.5	23.4	415	2	I58144	corlicotriopin-rele	
C 47	50.5	23.4	444	2	A48260	corlicotriopin-rele	
C 48	50.5	23.4	444	2	S31300	regulatory protein	
C 49	50.5	23.4	550	2	A64826	hybrid cluster 14F	
C 50	50.5	23.4	550	2	A10608	prismane protein h	
					G90748	probable prismane	

ALIGNMENTS

RESULT 1
AC2211
heme transport protein alr3242 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Strain: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AC2211
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriyama, T.;
Nakazawa, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2211
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-877 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA874941.1; PID:917132337; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr3242

Alignment Scores:	
pred. No.:	1 57
Score:	61.00
Percent Similarity:	55.56%
Best Local Similarity:	36.11%
Query Match:	28.37%
DB:	2
length:	877
Matches:	13
Conservative:	7
Mismatches:	16
Indels:	0
Gaps:	0

A; Reference number: SI29//; MUID:91092433; PMID:2265/11

Score:	54.50	Matches:	12
--------	-------	----------	----

Percent Similarity:	62.86%	Conservative:	10
Best Local Similarity:	34.29%	Mismatches:	5
Query Match:	25.23%	Indels:	8
DB:	2	Gaps:	1

US-09-198-779B-1_COPY_1_121 (1-121) x B44110 (1-2110)

QY 107 GTCCGCTCATTTATACACATTATAACACAACGCACATGGATCAGACCCTTCATTT 48
:::||||| ::||| ||||| ||
db 2033 LeuLeuValGIugInAlaSerValIleLeuArgThrIleAspAlaSpArgSerPhe 20

QY	47	ATC-----	AGCATGGGCAGCGTCGATCTGTCCACC	18
			:::	
Db	2053	IleglUTyrglYleuaspserIeuglYmetIeuglmetargThr		2067

RESULT 9
A70668
mycoglossate synthase (EC 3.3.1.11) = *Mycobacterium tuberculosis*

C:\Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:\Accession: A70668

Comnor, R. J.; Davies, R.; Cole, S. T.; Rösch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rutter, K.; Seeger, K.; Skelton, S.; Squares, S.

A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:5634230
A:Accession number: A70660

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-2111 <COL>
A:Accession: AF000000.1 CD_703859.1 NID_000017.1

A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: mas

name homology [acyl-carrier-protein] S-malonyltransferase homology
C:Keywords: acyltransferase; carrier protein; coenzyme A; phosphotransferase
E:27.4.26/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
F:534.4815/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology

F.1444-1733/Domain: long-chain alcohol dehydrogenase homology <LADH>
F.1765-1945/Domain: short-chain alcohol dehydrogenase homology <SADH>
F.2016-2096/Domain: acyl carrier protein homology <ACP1>

Pred. No.:	15,2	Length:	211
Score:	54,50	Matches:	12
Percent Similarity:	62,86	Conservative:	10
Best local Similarity:	34,29	Mismatches:	8
Query Match:	25,23	Indels:	5
DB:	2	Gaps:	1

US-09-198-779B-1_COPY_1_121 (1-121) x A70668 (1-2111)

QY	107	GCCTCGCTCAATTATACACACATTAAATACACACGACACAMTGATCAGGACCGTCATT	48
	::: :::	::: :::	
Db	2034	LeuLeuValGluGlnAlaSerValIleLeuArgArgThrIleAspAlaAspArgSerPhe	2055

QY	47	ATC-----ACCATG66CAGCGTCGATCTGTCCACC	18
		::	
		:::::	
Db	2054	IleGIuTYrGIyLeuAspSerIeuGlumetLeuGlumetaArgThr	2066

RESULT 10
C866926

probable mycocerosic synthase [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae

C:Colle S T : Eijlmeijer K : Tamme K D : Whorwell N P : Whorwell
C:Accession : C86926
C:Update : 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-May-2001

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd
 nam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001.

A: Authors: Ruter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.
A: Title: Massive gene decay in the leprosy bacillus.
A: Reference number: A86909; MUID:21128732; PMID:11234002
A: Accession: C86926

A: Molecule type: DNA
A: Residues: 1-2116 <STO>
A: Cross-references: GB:AL450380; NID:q13092517; PDB:GSPDB:GM001447.1; GSPDB:GM001447.1

C1:Gene:mas
 A:Gene:mas
 C:Superfamily: mycoerotic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I
 C:Superfamily: [acyl-carrier-protein] S-malonyltransferase homology
 C:Superfamily: [acyl-carrier-protein] S-malonyltransferase homology

Alignment Scores:
Pred. No.: 15.

Score:	24.50	Matches:	12
Percent Similarity:	62.86%	Conservative:	10
Best Local Similarity:	34.29%	Mismatches:	8
Query Match:	25.23%	Indels:	5
DB:	2	Gaps:	1

US-09-198-779B-1_COPY_1-121 (1-121) x C86926 (1-2116)

QY 107 GTCTGCTCAATTATACACATTATTAACACACGACCAATGATCGAGCCGTCATT 48
:::||||: ::::||| ::|||::|::| |::|::| |
Db 2032 LeuLeuValGluGlnAlaSerValIleLeuArgArgThrIleAspAlaAspArgSerPhe 2051

QY 47 ATC-----AGCATGGGACGGCTGATCTGTCCACC 18
||| |||:|||| :|||:| |||
Db 2052 IleglUTyrgLYLeuAspserLeucilgYmetLeuGlumetArgThr 2066

RESULT 11
522652 transcription factor Brn-2 - African clawed frog

C:Species: *Xenopus laevis* (African clawed frog)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S22652

Nucleic Acids Res. 20, 1993, 1992.
A:Title: Nucleotide sequence of XLPOU3 cDNA, a member of the POU domain gene family e
;Reference number: S22652; MUID:92253425; PMID:1579504

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-382 <BAL>

A: Note: this sequence was submitted to the EMBL Data Library, March 1991
C: Superfamily: transcription factor Brn-1; homeobox homology; POU domain
Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;208-275/Domain: POU domain homology <POU>
F;294-350/Domain: homeobox homology <HOX>

Alignment Scores:	1		
Pred. No.:	17.6	Length:	382
Score:	54.00	Matches:	10

Percent Similarity:	30.32%
Best Local Similarity:	43.488%
Query Match:	25.00%
DB:	1

US-09-198-779B-1_COPY_1_121 (1-121) x S22652 (1-382)

93 TACACATTATTAACACAAGCAACATGGATCAGGACCGTCATTATACGCATGGCCAG 3
:: ::||| ||| ||||||| |||:: |||||

QY 33 CGTCGATCT 25

Db 166 ArgAspSer 168

Alignment Scores:

A;Experimental source: strain Delta H

C:Genetics: A:Gene: MTH1603
A:Start codon: TTG
C:Superfamily: acetate-CoA ligase homology
C:11-400/Domain: acetate-CoA ligase homology #status atypical <ACL>

Alignment Scores:	
Pred. No.:	24 9
Score:	53.00
Percent Similarity:	66.67%
Best Local Similarity:	50.00%
Query Match:	24.65%
DB:	2
Length:	400
Matches:	9
Conservative:	3
Mismatches:	6
Indels:	0
Gaps:	0

US-09-198-779B-1_COPY_1_121 (1-121) x B69081 (1-400)

```

Oy      26 GATGACCGTGGCCCATGCTGATTAATGGACGGCTCTGATCCATTGTTGGTTGG 79
        ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      256 AspaspGlucysProcygInGlutIleuAspProGluIuAspProIeuPheIleu 273

```

RESULT 20
M34969

hypothetical protein T12G3.2 - *Caenorhabditis elegans*

Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T24868
R: Sims, M.
submitted to the EMBL Data Library, January 1996
A/Reference number: Z19945

Alignment Scores:

Pred. No.:	25.2	length:	922
Score:	53.00	Matches:	14
Percent Similarity:	61.29%	Conservative:	5
Best local Similarity:	45.16%	Mismatches:	6
Query Match:	24.54%	Indels:	6
DB:	2	Gaps:	2

US-09-198-779B-1_COPY_1_121 (1-121) x T24868 (1-928)

```

Oy 105 CCGGTCGAATTATACACATTATATACACACG-----AACCAATGGATCA 61
    |||:::||||| ::| ||| ||||| |||||
Db 895 ProSerGlnLeuProSerProAsnGlnThrThrIleProHisMetTyraAsnAsnGlyIle 91

```

```

Oy      60  GGACCGTCATTATCAGCATGGGAGCGTCGA  28
          |||  |||||::|||  |||:::
Db      915  ---PrometiletyrGluHisHisGlnGln  924

```

RESULT 21

hypothetical protein PFB0540w - malaria parasite (*Plasmodium falciparum*)

C:Species: *Plasmodium falciparum*
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C:Accession: D11612
R:Gardner, M.J., Felleklein, H., Carucci, D.J., Cummings, L.M., Aravind, L., Kocin, E.V.,
R. Perla, M., Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O., Smith, H.O.
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite *Plasmodium falciparum*.
Reference number: A71600; MUID:99021743; PMID:9804551

A;Cross-references: GB:AE001401; GB:AE001362; MID:g3845209; PIDN:AAC71897.1; PID:g3845209
A;Experimental source: clone 3D
C;Genetics:
A;Gene: PFB0540w

Alignment Scores:	
Pred. No.:	25,4
Score:	53,00
Percent Similarity:	53,85%
Best Local Similarity:	38,46%
Query Match:	24,54%
DB:	2
Length:	1844
Matches:	10
Conservative:	4
Mismatches:	12
Indels:	0
Gaps:	0

US-09-198-779B-1_COPY_1_121 (1-121) x D71612 (1-1844)

```

QY 90 AACATTATAACACCAACGAACAATGGATCAGGACCGTCCATTATATCAGCATGGGACGGT 31
    ||| ||||| ||||| ::| ||||| ::|
Db 881 ASnASnASnASnASnASnASnASnASnASnASnASnASnASnASnASnASnASnASnASn 90
    ASnASnASnASnASnASnASnASnASnASnASnASnASnASnASnASnASnASnASnASn

```

```

QY      30 CGATCTGTCCACCGAGGC 13
          :: ::::::::::
Db      901 GlnGlyIleHisArgGly 906

```

RESULT 22

eyelid - fruit fly (*Drosophila melanogaster*)

C:Species: *Urosalpinx maculosa* (L.)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: T13049
R:Treisman, J.E.; Luk, A.; Rubin, G.M.; Heberlehn, U.
Submitted to the EMBL Data Library, March 1998
A:Reference number: Z17592

C;Keywords: DNA binding

Alignment Scores:	
Pred. No.:	25, 6
Score:	53, 00
Percent Similarity:	78, 57%
Best Local Similarity:	71, 43%
Query Match:	24, 54%
DB:	2
Length:	2715
Matches:	10
Conservative:	1
Mismatches:	3
Indels:	0
Gaps:	0

US-09-198-779B-1_COPY_1_121 (1-121) X T13049 (1-2715

Qy 84 AATACACACGACCATGGATCAGGACCGTCATTATCAG 43
 ||||| ::||| ||||| ||||| , ||
 Db 46 AsnAsnAsnSerAsnAsnGlySerAspProSerIleGln 55

RESULT 2

probable drug resistance protein [imported] - *Sinorhizobium meliloti* (strain 1021) ma

C:Species: *Sinorhizobium meliloti*
C:Date: 24-Aug-2001 #sequence_revision: 24-Aug-2001 #text_change: 30-Sep-2001
C:Accession: G533792
R:Barbanel, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Bartoy-Hubler, F.;
Kelman, S.; Keeling, D.H.; Palm, C.; Peck, M.C.; Stutzki, R.; Wells, D.H.; Yen, P.
Proc. Natl. Acad. Sci. U.S.A. 98: 9883-9888, 2001
Affile: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meli*
A:Reference number: A95262; MUID: 21396509; PMID: 11441432


```

Hypothetical protein YII055c - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 19-Apr-2002
C:Accession: S48424
R:Smith, V.
submitted to the EMBL Data Library, September 1994
A:Reference number: S48407
A:Accession: S48424
A:Molecule type: DNA
A:Residues: 1-627 <SMI>
A:Cross-references: GB:247047; EMBL:Z38060; NID:g603997; PID:g763291; GSPDB:GN00009; MIF
C:Genetics:
A:Gene: MIPS:YII055c
A:Cross-references: SGD:S0001317
A:Map position: 9L

Alignment Scores:
Pred. No.: 42.1 Length: 627
Score: 51.50 Matches: 11
Percent Similarity: 64.29% Conservative: 7
Best Local Similarity: 39.29% Mismatches: 7
Query Match: 23.84% Indels: 3
DB: 2 Gaps: 1

US-09-198-779B-1.COPY.1.121 (1-121) x S48424 (1-627)
OY 96 TTATGACACATTAT-----ACACAGCAACATGATGACGACGTCACATTAT 46
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 329 LeuYrAnleuAsnMeAlAsersnsernsnAsnnglyAsnIleProHThrSer 348
OY 45 CAGCATGGCGCAGCGTCGATCTGTC 22
::||| |||:::
DB 349 ThrAnGIyAspAspArgAlaLeu 356

RESULT 28
T24216
chromosome condensation protein homolog DPr-27 - Caenorhabditis elegans
N:Alternate names: protein R13G10.1
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Jun-2000
C:Accession: T24216; A55095
R:Gardner, A.
submitted to the EMBL Data Library, August 1994
A:Reference number: Z19857
A:Accession: T24216
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1469 <NLI>
A:Cross-references: EMBL:Z35602; PIDN:CA84669.1; GSPDB:GN00021; CESP:R13G10.1
A:Experimental source: clone R13G10
R:Chuang, P.T.; Albertson, D.G.; Meyer, B.J.
Cell 79, 459-474, 1994
A:Title: DPr-27: a chromosome condensation protein homolog that regulates Caenorhabditis
A:Reference number: A55095; MUID:95042743; PMID:7954812
A:Accession: A55095
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-1132; 'G', 1134-1469 <CHU>
A:Cross-references: GB:I5274; NID:g529384; PIDN:AA62647.1; PID:g529385
A:Note: authors translated the codon GAT for residue 1133 as Gly
C:Genetics:
A:Gene: CESP:R13G10.1
A:Map position: 3
A:Introns: 142/3; 176/3; 296/2; 548/2; 627/3; 697/2; 847/3; 993/3; 1086/2; 1202/3; 1383/3
C:Superfamily: chromosome segregation protein SMC1

Alignment Scores:
Pred. No.: 42.6 Length: 1469
Score: 51.50 Matches: 12
Percent Similarity: 57.69% Conservative: 3
Best Local Similarity: 46.15% Mismatches: 8
Query Match: 23.84% Indels: 3
DB: 2 Gaps: 1

```

```

US-09-198-779B-1_COPY_1_121 (1-121) x T24216 (1-1469)
OY 71 ACATGATCAGACCGCTCATTTATC-----ACATGGCAGCGTCGATCTGTCC 21
    ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10 ThrsrAspAspAspArgProTyrAlaSpHrAspSerMetProGluValAspLeuasp 29
    ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 20 ACCGAGCGCTAGACGGAAA 3
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 30 ValAspArgAlaArgAlaGln 35
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 29
E70522
probable polyketide synthase - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: E70522
R:COLE, S.T.; BROSCH, R.; PARKHILL, J.; GARNIER, T.; CHURCHER, C.; HARRIS, D.; GORDON, J.; CONNOR, R.; DAVIES, R.; DEVLIN, K.; FELTWELL, T.; GENTILES, S.; HAMLIN, N.; HOLROYD, R.; RAJANDREEM, M.A.; ROGERS, J.; RUTTER, S.; SEEGER, K.; SKELTON, S.; SQUARES, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: E70522
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-2126 <COL>
A:Cross-References: GB:Z57188; GB:AL133456; NID:q3261805; PIDN:CAB10012.1; PID:g22248
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: pks2
C:Superfamily: mycosiderosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I
nase homology; [acyl-carrier-protein] S-malonyltransferase homology
C:Keywords: carrier protein
F:46-445/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
F:553-833/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F:1451-1739/Domain: long-chain alcohol dehydrogenase homology <LADH>
F:1772-1952/Domain: short-chain alcohol dehydrogenase homology <SADH>
F:2044-2109/Domain: acyl carrier protein homology <ACP>

Alignment Scores:
Pred. NO.: 42.9 Length: 2126
Score: 51.50 Matches: 12
Percent Similarity: 65.52% Conservative: 7
Best Local Similarity: 41.38% Mismatches: 5
Query Match: 23.84% Indels: 5
DB: 2 Gaps: 1

US-09-198-779B-1_COPY_1_121 (1-121) x E70522 (1-2126)
OY 89 ACATTAATATACACACGAAACATGCATCGACGCGCC-----TTTATC 45
    ::||| ||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2055 SerLeuIleLeuArgTrgThrValAspProAspArgProLeuProGluTyrGlyLeuasp 2074
    ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 44 AGCATGGCAGCGTCGATCTGTCCACC 18
    ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2075 SerLeuGlyAlaLeuGluLeuArgThr 2083
    ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 30
T04971
hypothetical protein T16L1.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
C:Accession: T04971
R:Bevan, M.; Obermayer, B.; Deutschenbaur, S.; Piravandi, E.; Hohnel, J.; Mewes, H.
submitted to the Protein Sequence Database, November 1998
A:Reference number: Z15393
A:Accession: T04971
A:Molecule type: DNA
A:Residues: 1-371 <BEV>
A:Cross-References: EMBL:AL031394
A:Experimental source: cultivar Columbia; BAC clone T16L1

```

C:Genetics:
 A:Map position: 4
 A:Introns: 69/1; 83/3; 123/3; 176/2; 201/2; 224/3; 275/3; 312/1; 333/1
 A>Note: T16L1.30
 C:Superfamily: Arabidopsis thaliana hypothetical protein T16L1.30

Alignment Scores:

Pred. No.:	49.7	Length:	371
Score:	51.00	Matches:	12
Percent Similarity:	60.87%	Conservative:	2
Best Local Similarity:	52.17%	Mismatches:	9
Query Match:	23.72%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779b-1_COPY_1_121 (1-121) x T04971 (1-371)

QY 19 GTGACAGATGACGCTGCTGCTGATTAATGAGCGCTCCTGATTCATTTGCTGT 78

Db 153 ValAspIysAspThrIleuProValIeuPheAsnProIeuSerPheHisPhePheArgMet 172

QY 79 GTTATTAAAT 87

Db 173 ValIleAsn 175

RESULT 31

Phosphatidate cytidyllyltransferase-like protein - Arabidopsis thaliana

N:Alternate names: protein T4C21.30

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: T47873

R:Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Catolico, L.; Artiguenave, F.; Sg

.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.

Submitted to the Protein Sequence Database, March 2000

A:Reference number: 224479

A:Accession: T47873

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-399 <CHO>

A:Cross-references: EMBL:AL162295

A:Experimental source: cultivar Columbia; BAC clone T4C21

C:Genetics:

A:Map position: 3

A:Introns: 81/3; 185/2; 249/1; 290/3; 335/2; 374/1

A>Note: T4C21.30

Alignment Scores:

Pred. No.:	49.7	Length:	399
Score:	51.00	Matches:	16
Percent Similarity:	52.78%	Conservative:	3
Best Local Similarity:	44.44%	Mismatches:	11
Query Match:	23.72%	Indels:	6
DB:	2	Gaps:	2

US-09-198-779b-1_COPY_1_121 (1-121) x T47873 (1-399)

QY 3 TTTCGCTTACCTCGGCGACATGACCGTCCCTGCTGATTAATGACGCTCTG 62

Db 254 TrpProThrIleLeuGlyGlyGln-----AlaHis-----TrpThrValGly 267

QY 63 ATTCATTGTCGTTGTTATTATTAAATGTTAAATGAGACACACA 110

Db 268 LeuValAlaIleLeuIleSerPheCysGlyIleIleAlaSerAspThr 283

RESULT 32

hypothetical protein E04A4.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T32605

R:Sammons, L.; Wohldmann, P.; Biewald, T.

submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid E04A4.

A:Reference number: 221199

A:Accession: T32605

A:Status: preliminary; translated from GR/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-433 <SAM>

A:Cross-references: EMBL:AF038611; PIDN:AAB92038.1; GSEDB:GN00022; CESP:E04A4.3

A:Experimental source: strain Bristol N2; clone E04A4

C:Genetics:

A:Gene: CESP:E04A4.3

A:Map position: 4

A:Introns: 21/2; 113/1; 147/3; 190/1; 283/2; 345/3; 382/3; 418/2

Alignment Scores:

Pred. No.:	49.8	Length:	433
Score:	51.00	Matches:	10
Percent Similarity:	57.89%	Conservative:	1
Best Local Similarity:	52.63%	Mismatches:	8
Query Match:	23.72%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779b-1_COPY_1_121 (1-121) x T32605 (1-433)

QY 20 TGGACAGATGACGCTGCTGCTGATTAATGAGCGCTCCTGATTCATTTGCTGT 76

Db 324 TrpGlyGlyArgArgCysProCysIeuLeuValAspGlyIuaAlaIeuVal 342

RESULT 33

transcription factor POU-1 - planarian (Dugesia japonica)

C:Species: Dugesia japonica

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jun-2000

C:Accession: JQ2010

R:Orli, H.; Agata, K.; Watanabe, K.

Biochem. Biophys. Res. Commun. 192, 1395-1402, 1993

A:Title: POU-domain genes in planarian Dugesia japonica: the structure and expression

A:Reference number: JQ2010; MUID:93282851; PMID:8099480

A:Accession: JQ2010

A:Molecule type: mRNA

A:Residues: 1-559 <ORI>

A:Cross-references: DDBJ:DJ2924; NID:9217311; PIDN:BAA02308.1; PID:9217312

A:Experimental source: strain GI

C:Genetics:

A:Gene: Dpou1

C:Superfamily: planarian transcription factor POU-1; homeobox homology; POU domain ho

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:266-333/Domain: POU domain homology <POU>

F:352-408/Domain: homeobox homology <HOX>

Alignment Scores:

Pred. No.:	50	Length:	559
Score:	51.00	Matches:	8
Percent Similarity:	58.33%	Conservative:	6
Best Local Similarity:	33.33%	Mismatches:	10
Query Match:	23.61%	Indels:	0
DB:	1	Gaps:	0

US-09-198-779b-1_COPY_1_121 (1-121) x JQ2010 (1-559)

QY 105 CCTGCTCAATTATACACATTATACACAGCAATGATGACGCTCCATTAT 46

Db 534 ProArgSerPhePheMetIleYAsnAsnIleYerIasnGlyThrThrProThrLeuPhe 553

QY 45 CAGCATGGCGAG 34

Db 554 AspHisSerGln 557

RESULT 34

hypothetical protein B0024.14 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T18649

R:McMurray, A.


```

C.Species: Neurospora crassa
C.Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C.Accession: T49596
R.Schultze, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A.Reference number: Z25022
A.Accession: T49596
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-259 <SCH>
A.Cross-references: EMBL:AL355931; GSPDB:GN00116; NCSP:B3E4.90
A.Experimental source: BAC clone B3E4; strain OR74A
C.Genetics:
A:Gene: NCSP:B3E4.90
A:Map position: 6

Alignment Scores:
Pred. No.:      58.8          Length:      259
Score:         50.50        Matches:       10
Percent Similarity: 54.84%    Conservative: 7
Best Local Similarity: 32.26% Mismatches:     11
Query Match:    23.38%      Indels:         3
DB:             2           Gaps:            1

US-09-198-779B-1_COPY_1_121 (1-121) x T49596 (1-259)

QY      96  TTATACAACTTATTACACAAGCAACATGATCGAGCCGTCCATTATTCAGCATGG 37
       ::::::::::::: ||| ||||| ::::::: |||||
Db      217  ILEHSAANGISySrgcIYTThrlnsnmsnnsnglyAnsglyLeuphExnhisgLy 236
QY      36  CAG-----CGTCGATCTGTCACCGCAGGC 13
       ||| ::::| | |
Db      237  ProleuSerValSerArgAspleuhisphegly 247

RESULT 43
B97980
dihydroorotate oxidase (EC 1.3.3.1) pyrD [imported] - Streptococcus pneumoniae (strain F
C.Species: Streptococcus pneumoniae
C.Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C.Accession: B97980
R.Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
ge, R.; LeBlanc, D.J.; Lee, L.N.; Leftowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; K
J. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A.Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A.Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A.Reference number: A97872; MUID:21429245; PMID:11544234
A.Accession: B97980
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-330 <KUD>
A.Cross-references: GB:AE007317; PIDN:AAK9670.1; PID:g15458470; GSPDB:GN00174
C.Genetics:
A:Gene: pyrD
C:Superfamily: dihydroorotate oxidase
C.Keywords: oxidoreductase

Alignment Scores:
Pred. No.:      59          Length:      330
Score:         50.50        Matches:      14
Percent Similarity: 56.00%    Conservative: 0
Best Local Similarity: 56.00% Mismatches:     10
Query Match:    23.38%      Indels:         1
DB:             2           Gaps:            1

US-09-198-779B-1_COPY_1_121 (1-121) x B97980 (1-330)

QY      86  TTATACACAACGAACATGATCGAGCCGTCCATTATTCAGCATGGCAGCGTCGAT 27
       ||||| ||| ||| ||| ||||| |||||
Db      251  leuIIeaTgGlnValAlaIslnrThrAspleuProllellleclgmetslglvalasp 270
QY      26  CTGTCACCGCAGGCT 12
       |||||||||

```

```

Db      271 ---SerThrGluAla 274

RESULT 44
S39535
corticotropic-releasing hormone receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999
C:Accession: S39535
R:Vita, N.; Laurent, P.; Lefort, S.; Chalou, P.; Lelias, J.M.; Kaghad, M.; le Fur, G.
FEBS Lett. 335, 1-5, 1993
A:Title: Primary structure and functional expression of mouse pituitary and human bra
A:Reference number: S39534; MUID:94063063; PMID:8243652
A:Accession: S39535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-415 <VIT>
A:Cross-references: EMBL:X72305; NID:9436120; PIDN:CA51053.1; PID:9436121
A:Note: the sequence from Fig. 1 is inconsistent with that from Fig. 3 in having an a
C:Keywords: G protein-coupled receptor; transmembrane protein

Alignment Scores:
Pred. No.:      59.2      Length:      415
Score:          50.50     Matches:      10
Percent Similarity: 68.75%  Conservative: 1
Best Local Similarity: 62.50%  Mismatches:  4
Query Match:    23.38%      Indels:      1
DB:             2          Gaps:          1

US-09-198-779B-1_COPY_1_121 (1-121) x S39535 (1-415)

OY      108 TGTCCTGCTCAATTATACACACATTAT--AACACACGACACATGCA 64
          |||||  ||  ::  |||||  |||||  |||||  |||||  |||||  |||||
Db      68 CysProAlaPhePheTyrGlyValaIrgTyrAsnThrTrpAsnAsnGly 83

RESULT 45
S18144
corticotropic-releasing factor receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
C:Accession: S18144
R:Chang, C.P.; Pearce, R.V.; O'Connell, S.; Rosenfeld, M.G.
Neuron 11, 1187-1195, 1993
A:Title: Identification of a seven transmembrane helix receptor for corticotropin-rel
A:Reference number: S18144; MUID:94099969; PMID:8274282
A:Accession: S18144
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-415 <RES>
A:Cross-references: GB:L25438; NID:9450298; PIDN:AAA16441.1; PID:9457615
C:Superfamily: glucagon receptor

Alignment Scores:
Pred. No.:      59.2      Length:      415
Score:          50.50     Matches:      10
Percent Similarity: 68.75%  Conservative: 1
Best Local Similarity: 62.50%  Mismatches:  4
Query Match:    23.38%      Indels:      1
DB:             2          Gaps:          1

US-09-198-779B-1_COPY_1_121 (1-121) x S18144 (1-415)

OY      108 TGTCCTGCTCAATTATACACACATTAT--AACACACGACACATGCA 64
          |||||  ||  ::  |||||  |||||  |||||  |||||  |||||  |||||
Db      68 CysProAlaPhePheTyrGlyValaIrgTyrAsnThrTrpAsnAsnGly 83

Search completed: April 23, 2003, 12:07:59
Job time : 16.0833 secs

```

THIS PAGE BLANK (USPTO)